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/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD29, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 83.3%; Score 17.6; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GGACTTTTGTGTTTGTGTTT 4483
Db 1 GTAGTTTGTGTTTGTGTTT 24

RESULT 942
LOCUS AU264231 26 bp mRNA linear EST 10-MAY-2002
DEFINITION AU264231 VS Dictyostelium discoideum cDNA VSD54 5', mRNA
ACCESSION AU264231
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 26)
AUTHORS Urushihara,H., Morio,T., Saito,T., Korihi,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hidekobio1.tsukuba.ac.jp.
Location/Qualifiers
1. 26
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD54"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match
Best Local Similarity 80.0%; Score 17.6; DB 1; Length 26;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5473 TTTTGTAAAGATAATTTT 5497
Db 1 TTTTGTAAAGATAATTTT 5497

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Db 25 TTTTGTATGATGATATTTT 1

RESULT 943
LOCUS CF302323 26 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-L19, b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-L19, mRNA sequence.
ACCESSION CF302323
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 26)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bnhahm@gsbto.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-L19"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match
Best Local Similarity 83.3%; Score 17.6; DB 1; Length 26;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4465 TTTTGTGTTTGTGTTT 4488
Db 1 TTTTGTGTTTGTGTTTCT 24

RESULT 944
LOCUS AZ422541 26 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0201614F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM020161 F, genomic survey sequence.
ACCESSION AZ422541
VERSION AZ422541.1 GI:10546554
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

```

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 8412 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0201 row: 6 column: 14
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UDGCM0201G14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UDGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 8.4e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4468 TTTTCTTTTCTGCTGAG 4491
 Db 1 TGTCTTTTCTGCTGAG 24

RESULT 945
 EX550767 27 bp mRNA linear EST 10-OCT-2003
 LOCUS BX550767 Glossina morsitans adult infected gut Glossina
 DEFINITION morsitans morsitans cDNA clone Tse114f12_p1c, mRNA sequence.
 ACCESSION BX550767
 VERSION BX550767.1 GI:33374306
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE
 1 (bases 1 to 27)
 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes

JOURNAL
 MEDLINE 22881942
 PUBMED 14519198
 Genome Biol. 4 (10), R63 (2003)

COMMENT

Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.
 Location/Qualifiers

FEATURES

source

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1..27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

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Query Match 0.2%; Score 17.6; DB 1; Length 27;
 Best Local Similarity 83.3%; Pred. No. 9e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTCTTTTCTTTT 4482
 Db 4 TAGATAGTTTCTTTTCTTTT 27

RESULT 946
 EX550946 27 bp mRNA linear EST 10-OCT-2003
 LOCUS BX550946 Glossina morsitans morsitans adult infected gut Glossina
 DEFINITION morsitans morsitans cDNA clone Tse115f11_p1c, mRNA sequence.
 ACCESSION BX550946
 VERSION BX550946.1 GI:33374735
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE
 1 (bases 1 to 27)
 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes

JOURNAL
 MEDLINE 22881942
 PUBMED 14519198
 Genome Biol. 4 (10), R63 (2003)

COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix g1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.
 Location/Qualifiers

FEATURES

source

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1..27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"

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/db_xref="taxon:37546"
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/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTT TTTT TTTT TTTT TTTT 4482
DB 4 TAGATAGTT TTTT TTTT TTTT TTTT 27

RESULT 947
BX551145 27 bp mRNA linear EST 10-OCT-2003
LOCUS BX551145 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans CDNA clone Tse115h03_p1c, mRNA sequence.
ACCESSION BX551145
VERSION BX551145.1 GI:33375002
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
Location/Qualifiers
1..27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

FEATURES
source
1..27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse115h03_p1c"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTT TTTT TTTT TTTT TTTT 4482
DB 4 TAGATAGTT TTTT TTTT TTTT TTTT 27

RESULT 948
BX551153 27 bp mRNA linear EST 10-OCT-2003
LOCUS BX551153 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans CDNA clone Tse115h08_p1c, mRNA sequence.
ACCESSION BX551153
VERSION BX551153
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)

JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
Location/Qualifiers
1..27
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/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTT TTTT TTTT TTTT TTTT 4482
DB 4 TAGATAGTT TTTT TTTT TTTT TTTT 27

RESULT 949
BX551505 27 bp mRNA linear EST 10-OCT-2003
LOCUS BX551505 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans CDNA clone Tse119a03_p1c, mRNA sequence.
ACCESSION BX551505
VERSION BX551505.1 GI:33375704
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina

REFERENCE
AUTHORS
TITLE
Adult midgut expressed sequence tags from the tsetse fly Glossina

morisiens morisiens and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
JOURNAL MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N

morbitans morbitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), Re3 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2NW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES	Location/Qualifiers
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/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
.brucei"

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Query Match	0.2%	Score 17.6;	DB 1;	length 27;
Best Local Similarity	83.3%;	Pred. No. 9e+02;		
Matches 20;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

OY	4459	TGACACTTTTCTTTTTTTTTTTTTTT	4482
D6	4	TAGATAGTTTCTTTTTTTTTTTTTTT	27

RESULT 950

LOCUS	27 bp	mRNA	linear	EST 10-OCT-2003
DEFINITION	BX551552	<i>Glossina morsitans morsitans</i> adult infected gut <i>Glossina morsitans morsitans</i> CDNA clone Tsell19c07_p1c, mRNA sequence.		

ACCESSION	BX551552
VERSION	BX551552.1
	GI:33375771

SOURCE ORGANISM	Glossina morsitans morsitans
Glossina morsitans morsitans	

REFERENCE

TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina* Hamilton, J., Soares, M.B., Ronaldo, M.F., Lehane, S. and Hall, N.

JOURNAL of Genome Biol. 4 (10), R63 (2003)

COMMENT	Contact: Hall N

Hinxton, Cambridge, CB10 1SA, UK

School of Biological Sciences,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES	Location/Qualifiers
source	1. .27

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location/Qualifiers
1.27
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Query Match	0.28;	Score 17.6;	DB 1;	Length 27;
Best Local Similarity	83.3%;	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4;
				Indels 0;
				Gaps 0;

Oy	4459	TGACACTTTT	TTTTTTTTTTTT	TTTT	4482
Db	4	TAGATAGTTT	TTTTTTTTTTTT	TTTT	27

RESULT 951
BX551708

LOCUS	27 bp	linear	EST 10-OCT-2003
DEFINITION	EX551708	<i>Glossina morsitans morsitans</i> adult infected gut <i>Glossina morsitans morsitans</i> cDNA clone Tseilic02_p1c, mRNA sequence.	

ACCESSION	BX51708
VERSION	BX51708.1
	GI:33376038

SOURCE
ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.

REFERENCE AUTHORS TITLE	1 (bases 1 to 27)
Lehane, M. J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina</i>

JOURNAL
Genome Biol. 4 (10), R63 (2003)

PUBMED 14519198
COMMENT Contact: Hall N

The Sanger Institute The Wellcome Trust Genome
Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact
Prof. M.J. Lehane
School of Biological Sciences

University of Wales,
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES	Location/Qualifiers
source	1. .27

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1..27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
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/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe, EST from adult gut infected with
T. brucei"

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Query Match	0.2%;	Score 17.6;	DB 1;	Length 27;
Best Local Similarity	83.3%;	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4;
			Indels	0;
			Gaps	0;

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OY      4459 TGGACTTTTCTTTTTTTTTTTT 4482
        ||| ||||| ||||| ||||| |||||
DB      4 TAGATAGCTTTTCTTTTTTTTTTTT 27

RESULT 952
LOCUS   BK551731
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

FEATURES
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        location/Qualifiers
            1..27
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                /mol_type="mRNA"
                /sub_species="morsitans"
                /db_xref="taxon:37546"
                /clone="Tseilid03_pic"
                /tissue_type="adult infected gut"
                /clone_fids="Glossina morsitans morsitans adult infected gut"
                /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match          0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY      4459 TGGACTTTTCTTTTTTTTTTTT 4482
        ||| ||||| ||||| ||||| |||||
DB      4 TAGADAGCTTTTCTTTTTTTTTTTT 27

RESULT 953
LOCUS   BK551875
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BKS51875 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tseil20c06_pic, mRNA sequence.

BKS51875.1 GI:33376196
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hal N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.
location/Qualifiers
    1..27
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        /clone_fids="Glossina morsitans morsitans adult infected gut"
        /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

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REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
1. (bases 1 to 27)	Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198	
CONTACT:	Hall N					
UNIT:	The Sanger Institute The Wellcome Trust Genome Campus					
ADDRESS:	Hinxton, Cambridge, CB10 1SA, UK					
REQUEST FOR CLONES:	please contact: Mike Lehane					
PROF. M.J. LEHANE						
SCHOOL OF BIOLOGICAL SCIENCES,						
BANGOR LL57 2UW						
ALL CLONES WITH SUFFIX gic	are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.					
FEATURES	source	location/Qualifiers				
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Matches	20;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;	
4459	4459	4459	4459	4459	4459	4459
4	TAGATAGT	TTTTTTTTTTTTTTTTTT	TTTT	27		
RESULT 954						
BX551974						
LOCUS	27 bp	mRNA	linear	EST 10-OCT-2003		
DEFINITION	BX551974	Glossina morsitans morsitans adult infected gut	Glossina morsitans morsitans	cDNA clone Tse120H2.pic, mRNA sequence.		
ACCESSION	BX551974					
VERSION	BX551974.1	GI:33376288				
KEYWORDS	EST.					
SOURCE	Glossina morsitans morsitans					
ORGANISM	Glossina morsitans morsitans					
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.					
AUTHORS	1 (bases 1 to 27)					
TITLE	Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.					
JOURNAL	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes					
MEDLINE	Genome Biol. 4 (10), R63 (2003)					
PUBMED	22881942					
COMMENT	14519198					
CONTACT:	Hall N					
UNIT:	The Sanger Institute The Wellcome Trust Genome Campus					
ADDRESS:	Hinxton, Cambridge, CB10 1SA, UK					
REQUEST FOR CLONES:	please contact: Mike Lehane					
PROF. M.J. LEHANE						
SCHOOL OF BIOLOGICAL SCIENCES,						
BANGOR LL57 2UW						
ALL CLONES WITH SUFFIX gic	are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.					

University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES

source

Location/Qualifiers

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Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

0.2%; Score 17.6; DB 1; Length 27;

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4482

4 TAGATAGTTT

27

Db

4459 TGACCTTTT

4482

4 TAGATAGTTT

27

RESULT 955

BX552003

LOCUS

DEFINITION

BX552003

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Hall N

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

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University of Wales,

Bangor LL57 2UW

All clones with suffix g1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from

the 3' end.

Location/Qualifiers

1..27

/organism="Glossina morsitans morsitans"

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Hall N

The Sanger Institute The Wellcome Trust Genome Campus

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end of the cDNA all pic reads are from

the 3' end.

Location/Qualifiers

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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All clones with suffix g1c are reverse primer reads starting at 5'

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the 3' end.

Location/Qualifiers

1..27

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Hall N

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All clones with suffix g1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from

the 3' end.

Location/Qualifiers

1..27

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

FEATURES

source

Location/Qualifiers

1..27

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Hall N

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

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School of Biological Sciences,

University of Wales,

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All clones with suffix g1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from

the 3' end.

Location/Qualifiers

1..27

/organism="Glossina morsitans morsitans"

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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

JOURNAL

MEDLINE

PUBMED

COMMENT

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Hinxton, Cambridge, CB10 1SA, UK

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University of Wales,

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All clones with suffix g1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from

the 3' end.

Location/Qualifiers

1..27

/organism="Glossina morsitans morsitans"

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/db_xref="taxon:37546"

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KEYWORDS	EST.
SOURCE	Glossina morsitans morsitans
ORGANISM	Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina. 1 (bases 1 to 27)
REFERENCE	Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
AUTHORS	Genome Biol. 4 (10), R63 (2003) 22881942
JOURNAL	14519198
MEDLINE	Contact: Hall N
PUBMED	Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2NW
FEATURES	All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
source	Location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="RNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tse127g01_plc" /islane_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
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Best Local Similarity	83.3%; Pred. No. 9e+02;
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cy	4459 TGCACCTTTTTTTTTTTTTTTTTT 4482 TTTTTTTTTTTTTTTTTT 4 TAGATAGTTTTTTTTTTTTTTTTTT 27
Db	
RESULT 958	
BX553354	27 bp mRNA linear EST 10-OCT-2003
LOCUS	BX553354
DEFINITION	BX553354 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse128n1_plc, mRNA sequence.
ACCESSION	BX553354
VERSION	BX553354.1 GI:33377529
KEYWORDS	EST.
SOURCE	Glossina morsitans morsitans
ORGANISM	Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina. 1 (bases 1 to 27)
REFERENCE	Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
AUTHORS	Genome Biol. 4 (10), R63 (2003) 22881942
JOURNAL	14519198
MEDLINE	Contact: Hall N
PUBMED	Pathogen Sequencing Unit
COMMENT	

The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
SOURCE
location/Qualifiers
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/clone_idb="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4459 TGGACTTTTTTTTTTTTTTTTTT 4482
|||||
4 TAGATAGTTTTTTTTTTTTTTT 27

Db

RESULT 959
BX553476
LOCUS
DEFINITION BX553476 27 bp mRNA linear EST 10-OCT-2003
morsitans morsitans cDNA clone Tse129f12.pic, mRNA sequence.
ACCESSION BX553476
VERSION BX553476.1 GI:33377634
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane,M.J., Akroy,S., Gibson,W., Kethornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)

JOURNAL
MEDLINE
PUBMED
COMMENT

TITLE
CONTACT: Hall N
The Sanger Institute The Wellcome Trust Genome Camps
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
SOURCE
Location/Qualifiers
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Best Local Similarity	83.3%	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
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DB	4	TAGATAGTTT	TTTTTTTTTTT	27
RESULT 960				
LOCUS	BX553666	27 bp	mRNA	linear
DEFINITION	BX553666	Glossina morsitans morsitans adult infected gut	Glossina morsitans morsitans cDNA clone Tse12H08_p1c	mRNA sequence.
ACCESSION	BX553666			
VERSION	BX553666.1	GI:33377811		
KEYWORDS	EST.			
SOURCE	Glossina morsitans morsitans			
ORGANISM	Glossina morsitans morsitans			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
AUTHORS	Lehane, M.J., Akroy, S., Gibson, W., Kehornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
JOURNAL	Genome Biol.	4 (10),	R63 (2003)	
MEDLINE	22881942			
PUBMED	14519198			
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.			
FEATURES	Location/Qualifiers			
SOURCE	1..27			
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	/sub_species="morsitans"			
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	/note="country: Zimbabwe; EST from adult gut infected with T.brucei"			
Query Match	0.2%	Score 17.6;	DB 1;	Length 27;
Best Local Similarity	83.3%	Pred. No. 9e+02;		
Matches	20;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
QY	4459	TGCACTTTT	TTTTTTTTTTT	4482
DB	4	TAGATAGTTT	TTTTTTTTTTT	27
RESULT 961				
LOCUS	BX553766	27 bp	mRNA	linear
DEFINITION	BX553766	Glossina morsitans morsitans adult infected gut	Glossina morsitans morsitans cDNA clone Tse12H08_p1c	mRNA sequence.
ACCESSION	BX553766			
VERSION	BX553766.1	GI:33377811		
KEYWORDS	EST.			
SOURCE	Glossina morsitans morsitans			
ORGANISM	Glossina morsitans morsitans			
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.			
AUTHORS	Lehane, M.J., Akroy, S., Gibson, W., Kehornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.			
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes			
JOURNAL	Genome Biol.	4 (10),	R63 (2003)	
MEDLINE	22881942			
PUBMED	14519198			
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.			
FEATURES	Location/Qualifiers			
SOURCE	1..27			
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	/clone_lib="Glossina morsitans morsitans adult infected gut"			
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LOCUS	BX553766	27 bp	mRNA	linear	EST 10-OCT-2003
DEFINITION	BX553766 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse130e04_p1c, mRNA sequence.				
ACCESSION	BX553766				
VERSION	BX553766.1	GI:33377899			
KEYWORDS	EST.				
SOURCE	Glossina morsitans morsitans				
ORGANISM	Glossina morsitans morsitans				
REFERENCE	Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.				
AUTHORS	Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.				
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes				
JOURNAL	Genome Biol.	4	(10),	Re3	(2003)
MEDLINE	22881942				
PUBMED	14519198				
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tse130e04_p1c" /issue_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: zimbabwe; EST from adult gut infected with T.brucei"				
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Query Match	0.2%; Score 17.6;	DB 1;	Length 27;		
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Matches	20;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Ov	4459	TGGACTTTTTTTTTTTTTTTT	4482		
Db	4	TAGATAGTTTTTTTTTTTTTT	27		
RESULT 962					
BX554327					
LOCUS	BX554327	27 bp	mRNA	linear	EST 10-OCT-2003
DEFINITION	BX554327 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse14g09_p1c, mRNA sequence.				
ACCESSION	BX554327				
VERSION	BX554327.1	GI:33378417			
KEYWORDS	EST.				
SOURCE	Glossina morsitans morsitans				
ORGANISM	Glossina morsitans morsitans				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.				
AUTHORS	Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.				
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes				


```

RESULT 965      Db          4 TAGATAGTGTGTTTTTTT TTTT TTTT 27
LOCUS           BX555155
DEFINITION      BX555155 Glossina morsitans morsitans adult infected gut Glossina
                  morsitans morsitans cDNA clone Tse19g11_p1c, mRNA sequence.
ACCESSION       BX555155
VERSION         BX555155.1 GI:33379174
KEYWORDS        EST.
SOURCE          Glossina morsitans morsitans
ORGANISM        Glossina morsitans morsitans
AUTHORS         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Hippoboscidae; Glossinidae; Glossina.
REFERENCE       1 (bases 1 to 27)
                Lehane,M.J., Akcoy,S., Gibson,W., Kephornou,A., Berriman,M.,
                Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
                Adult midgut expressed sequence tags from the tsetse fly Glossina
                morsitans morsitans and expression analysis of putative immune
                response genes
JOURNAL         Genome Biol. 4 (10), R63 (2003)
MEDLINE         22881942
PUBMED         14519198
COMMENT         Contact: Hall N
                  Pathogen Sequencing Unit
                  The Sanger Institute The Wellcome Trust Genome Campus
                  Hinxton, Cambridge, CB10 1SA, UK
                  Request for clones, please contact: Mike Lehane
                  Prof. M.J.Lehane
                  School of Biological Sciences,
                  University of Wales,
                  Bangor IL57 2UW
                  All clones with suffix q1c are reverse primer reads starting at 5'
                  end of the cDNA all p1c reads are from
                  the 3' end.
FEATURES
source          location/Qualifiers
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                /tissue_type="adult infected gut"
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                T.brucei"
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Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches        20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy             4459 TGAAGCTTTTGTGTTTTTTT 4482
                ||| ||||| ||||| |||||
Db             4 TAGATAGTGTGTTTTTTT TTTT TTTT 27

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FEATURES	source	Location/Qualifiers
JOURNAL	Genome Biol. 4 (10), R63 (2003)	
MEDLINE	22881942	
PUBMED	14519198	
COMMENT	<p>Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW</p> <p>All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.</p>	
FEATURES	1..27	
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Query Match	0.2%; Score 17.6; DB 1; Length 27;	
Best Local Similarity	83.3%; Pred. No. 9e+02;	
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	4459 TGGACTTTTTTTTTTTTTTTTTT 4482	
Db	4 TAGATAGTTTTTTTTTTTTTTTTT 27	
RESULT 967		
LOCUS	BX555500 27 bp mRNA linear EST 10-OCT-2003	
DEFINITION	BX555500 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21a01_plc, mRNA sequence.	
ACCESSION	BX555500	
VERSION	BX555500.1 GI:33379491	
KEYWORDS	EST.	
SOURCE	Glossina morsitans morsitans	
ORGANISM	Glossina morsitans morsitans	
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.	
AUTHORS	1 (bases 1 to 27) Lehane,M.J., Akroy,S., Gibson,M., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.	
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes	
JOURNAL	Genome Biol. 4 (10), R63 (2003)	
MEDLINE	22881942	
PUBMED	14519198	
COMMENT	<p>Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW</p>	

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

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Location/Qualifiers
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4482

Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 27

RESULT 968

BX555567

LOCUS BX555567 27 bp mRNA linear EST 10-OCT-2003
DEFINITION BX555567 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21d12_plc, mRNA sequence.

ACCESSION BX555567

VERSION BX555567.1 GI:33379550
KEYWORDS EST.

SOURCE

ORGANISM

Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 27)

Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

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Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

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Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

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Genome Biol. 4 (10), R63 (2003)

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Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4482

Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 27

RESULT 969

BX555594

LOCUS BX555594 27 bp mRNA linear EST 10-OCT-2003
DEFINITION BX555594 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21f02_plc, mRNA sequence.

ACCESSION BX555594

VERSION BX555594.1 GI:33379576
KEYWORDS EST.

SOURCE

ORGANISM

Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 27)

Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

Genome Biol. 4 (10), R63 (2003)

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Genome Biol. 4 (10), R63 (2003)

Query Match

0.2%; Score 17.6; DB 1; Length 27;

ORGANISM	Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina. 1 (bases 1 to 27)
REFERENCE	Lehane,M.J., Aksoy,S., Gibson,M., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
TITLE	JOURNAL MEDLINE PUBMED Genome Biol. 4 (10), R63 (2003) 22881942 14519198
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.
FEATURES	Location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tse23506_p1c" /tissue_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
Source	Query Match 0.2%; Score 17.6; DB 1; Length 27; Best Local Similarity 83.3%; Pred. No. 9e+02; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	4459 TGGACTTTTCTTTTTTTTTTTT 4482 Db 4 TAGATAGCTTTTCTTTTTTTT 27
RESULT 971	BX555864 27 bp mRNA linear EST 10-OCT-2003 LOCUS BX555864 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse23d05_p1c, mRNA sequence. BX555864 KEYWORDS BX555864.1 GI:33379834 SOURCE EST. ORGANISM Glossina morsitans morsitans Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina. 1 (bases 1 to 27)
REFERENCE	Lehane,M.J., Aksoy,S., Gibson,M., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
AUTHORS	JOURNAL MEDLINE PUBMED Genome Biol. 4 (10), R63 (2003) 22881942 14519198
TITLE	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK
COMMENT	

Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix plc are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

Location/Qualifiers

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/organism="Glossina morsitans morsitans"

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/note="country: Zimbabwe; EST from adult gut infected with T.Brucei"

Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 4 TAGATAGTTTTTTTTTTTTTTTTT 27

RESULT 972

LOCUS BX555901 27 bp mRNA linear EST 10-OCT-2003

DEFINITION BX555901 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse23f02_plc, mRNA sequence.

ACCESSION BX555901

VERSION BX555901.1 GI:33379871

KEYWORDS EST,

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippodrosocidae; Glossinidae; Glossina.

1 (bases 1 to 27)

Lehane,M,J., Aksoy,S., Gibson,W., Kerkhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

Location/Qualifiers

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"gut"
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T.brucei"

Query Match      0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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      ||| ||||| ||||| ||||| |||||
      4 TAGATAGCTTTTCTTTTCTTTTCTTTT 27

RESULT 973
LOCUS      BX555930          27 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION      BX555930 Glossina morsitans morsitans adult infected gut Glossina
ACCESSION      BX555930
VERSION      BX555930.1 GI:33379899
KEYWORDS
SOURCE      EST.
ORGANISM      Glossina morsitans morsitans
                Glossina morsitans morsitans
                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Hippoboscidae; Glossinidae; Glossina.
REFERENCE      1 (bases 1 to 27)
                Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
                Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
                Adult midgut expressed sequence tags from the tsetse fly Glossina
                morsitans morsitans and expression analysis of putative immune
                response genes
                Genome Biol. 4 (10), R63 (2003)
JOURNAL      MEDLINE
PUBMED      14519198
COMMENT      Contact: Hall N
                Pathogen Sequencing Unit
                The Sanger Institute The Wellcome Trust Genome Campus
                Hinxton, Cambridge, CB10 1SA, UK
                Request for clones, please contact: Mike Lehane
                Prof. M.J.Lehane
                School of Biological Sciences,
                University of Wales,
                Bangor LL57 2UW
                All clones with suffix q1c are reverse primer reads starting at 5'
                end of the cDNA all p1c reads are from
                the 3' end.

FEATURES
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                /organism="Glossina morsitans morsitans"
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                T.brucei"

Query Match      0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4459 TGCACCTTTTCTTTTCTTTTCTTTT 4482
      ||| ||||| ||||| ||||| |||||
      4 TAGATAGCTTTTCTTTTCTTTTCTTTT 27

RESULT 974
LOCUS      BX556112          27 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION      BX556112 Glossina morsitans morsitans adult infected gut Glossina

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ACCESSION	BX556112	morsitans morsitans cDNA clone Tse25a07_p1c, mRNA sequence.
VERSION	BX556112..1	GI:33380051
KEYWORDS	EST.	
SOURCE	Glossina morsitans morsitans	
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.	
REFERENCE	1 (bases 1 to 27)	
AUTHORS	Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.	
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes	
JOURNAL	Genome Biol.	4 (10), R63 (2003)
MEDLINE	22881942	
PUBMED	14519198	
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J.Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..27 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /db_species="morsitans" /db_xref="taxon:37546" /clone="Tse25a07_p1c" /tissue_type="adult infected gut" /clone_1kb="Glossina morsitans morsitans adult infected gut" /note="Country: Zimbabwe; EST from adult gut infected with T.brucei"	
FEATURES	Source	
Query Match	0.2%; Score 17.6; DB 1; Length 27;	
Best Local Similarity	83.3%; Pred. No. 9e+02;	
Matches	20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
CY	4459 TGACCTTTTTTTTTTTTTTTTT 4482	
DB	4 TAGATAGTTTTTTTTTTTTTTT 27	
RESULT 975		
EX556156		
LOCUS	BX556156 27 bp mRNA linear EST 10-OCT-2003	
DEFINITION	BX556156 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse25c09_p1c, mRNA sequence.	
ACCESSION	BX556156	
VERSION	BX556156.1	GI:33380093
KEYWORDS	EST.	
SOURCE	Glossina morsitans morsitans	
ORGANISM	Glossina morsitans morsitans Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.	
REFERENCE	1 (bases 1 to 27)	
AUTHORS	Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.	
TITLE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes	
JOURNAL	Genome Biol.	4 (10), R63 (2003)
MEDLINE	22881942	

FEATURES	SOURCE	LOCATION/Qualifiers
JOURNAL MEDLINE PUBMED COMMENT	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	
JOURNAL MEDLINE PUBMED COMMENT	Genome Biol. 4 (10), R63 (2003)	
JOURNAL MEDLINE PUBMED COMMENT	22881942	
JOURNAL MEDLINE PUBMED COMMENT	14519198	
JOURNAL MEDLINE PUBMED COMMENT	Contact: Hall N	
JOURNAL MEDLINE PUBMED COMMENT	Pathogen Sequencing Unit	
JOURNAL MEDLINE PUBMED COMMENT	The Sanger Institute The Wellcome Trust Genome Campus	
JOURNAL MEDLINE PUBMED COMMENT	Hinxton, Cambridge, CB10 1SA, UK	
JOURNAL MEDLINE PUBMED COMMENT	Request for clones, please contact: Mike Lehane	
JOURNAL MEDLINE PUBMED COMMENT	Prof. M.J.Lehane	
JOURNAL MEDLINE PUBMED COMMENT	School of Biological Sciences,	
JOURNAL MEDLINE PUBMED COMMENT	University of Wales,	
JOURNAL MEDLINE PUBMED COMMENT	Bangor LL57 2UW	
JOURNAL MEDLINE PUBMED COMMENT	All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.	
JOURNAL MEDLINE PUBMED COMMENT	Location/Qualifiers	
JOURNAL MEDLINE PUBMED COMMENT	1..27	
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JOURNAL MEDLINE PUBMED COMMENT	/mol_type="mRNA"	
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JOURNAL MEDLINE PUBMED COMMENT	/db_xref="taxon:37546"	
JOURNAL MEDLINE PUBMED COMMENT	/clone="Tse34g04_p1c"	
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JOURNAL MEDLINE PUBMED COMMENT	/clone_11b="Glossina morsitans morsitans adult infected gut"	
JOURNAL MEDLINE PUBMED COMMENT	/note="country: Zimbabwe; EST from adult gut infected with T.brucei"	
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JOURNAL MEDLINE PUBMED COMMENT	Best Local Similarity	83.3%; Pred. No. 9e+02; 4; Indels 0; Gaps 0;
JOURNAL MEDLINE PUBMED COMMENT	Matches 20; Conservative 0; Mismatches 0;	
JOURNAL MEDLINE PUBMED COMMENT	4459 TGACATTTTTTTTTTTTTTTT 4482	
JOURNAL MEDLINE PUBMED COMMENT	4 TAGATAGTTTTTTTTTTTTTTT 27	
JOURNAL MEDLINE PUBMED COMMENT	RESULT 980	
JOURNAL MEDLINE PUBMED COMMENT	LOCUS	
JOURNAL MEDLINE PUBMED COMMENT	BX558430	
JOURNAL MEDLINE PUBMED COMMENT	DEFINITION	BX558430 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse38e12_p1c, mRNA sequence.
JOURNAL MEDLINE PUBMED COMMENT	ACCESSION	BX558430
JOURNAL MEDLINE PUBMED COMMENT	VERSION	BX558430.1 GI:33365138
JOURNAL MEDLINE PUBMED COMMENT	KEYWORDS	EST.
JOURNAL MEDLINE PUBMED COMMENT	SOURCE	Glossina morsitans morsitans
JOURNAL MEDLINE PUBMED COMMENT	ORGANISM	Glossina morsitans morsitans
JOURNAL MEDLINE PUBMED COMMENT	REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
JOURNAL MEDLINE PUBMED COMMENT	AUTHORS	1 (bases 1 to 27)
JOURNAL MEDLINE PUBMED COMMENT	TITLE	Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M., Hamilton,J., Soares,C.B., Donald,M.F., Lehane,S. and Hall,N.
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Genome Biol. 4 (10), R63 (2003)
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	22881942
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	14519198
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Contact: Hall N
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Pathogen Sequencing Unit
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	The Sanger Institute The Wellcome Trust Genome Campus
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Hinxton, Cambridge, CB10 1SA, UK
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Request for clones, please contact: Mike Lehane
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Prof. M.J.Lehane
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	School of Biological Sciences,
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	University of Wales,
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	Bangor LL57 2UW
JOURNAL MEDLINE PUBMED COMMENT	JOURNAL MEDLINE PUBMED COMMENT	All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

REFERENCE
1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly *Glossina*
moritans moritans and expression analysis of putative immune
response genes

JOURNAL
MEDLINE
PUBMED
22881942
14519198

COMMENT

Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1..27
Location/Qualifiers

/organism="Glossina moritans moritans"
/mol_type="mRNA"
/sub_species="moritans"
/db_xref="taxon:37546"
/clone="Tse52f10.pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina moritans moritans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 0.2%; Score 17.6; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TCGACTTTTCTTTTCTTTTCTTTT 4482
DB 4 TAGATAGTTTTTTTTTTTTTTTTT 27

RESULT 984

BX562177

LOCUS BX562177 27 bp mRNA linear EST 10-OCT-2003

DEFINITION BX562177 Glossina moritans moritans adult infected gut Glossina
moritans moritans cDNA clone Tse5b09.pic, mRNA sequence.

ACCESSION BX562177 GI:33372299

VERSION BX562177.1 GI:33372299

KEYWORDS EST.

SOURCE Glossina moritans moritans

ORGANISM Glossina moritans moritans

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

AUTHORS 1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina*
moritans moritans and expression analysis of putative immune
response genes

JOURNAL
MEDLINE
PUBMED
22881942
14519198

COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane

School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1..27
Location/Qualifiers

/organism="Glossina moritans moritans"
/mol_type="mRNA"
/sub_species="moritans"
/db_xref="taxon:37546"
/clone="Tse5b09.pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina moritans moritans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 0.2%; Score 17.6; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TCGACTTTTCTTTTCTTTTCTTTT 4482
DB 4 TAGATAGTTTTTTTTTTTTTTTTT 27

RESULT 985

BX564083

LOCUS BX564083 27 bp mRNA linear EST 10-OCT-2003

DEFINITION BX564083 Glossina moritans moritans adult infected gut Glossina
moritans moritans cDNA clone Tse6f02.pic, mRNA sequence.

ACCESSION BX564083 GI:33431280

VERSION BX564083.1 GI:33431280

KEYWORDS EST.

SOURCE Glossina moritans moritans

ORGANISM Glossina moritans moritans

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

AUTHORS 1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina*
moritans moritans and expression analysis of putative immune
response genes

JOURNAL
MEDLINE
PUBMED
22881942
14519198

COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

REFERENCE All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1..27
Location/Qualifiers

/organism="Glossina moritans moritans"
/mol_type="mRNA"
/sub_species="moritans"
/db_xref="taxon:37546"
/clone="Tse6f02.pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina moritans moritans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 0.2%; Score 17.6; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TCGACTTTTCTTTTCTTTTCTTTT 4482
DB 4 TAGATAGTTTTTTTTTTTTTTTTT 27

RESULT 984
BX562177
LOCUS BX562177 27 bp mRNA linear EST 10-OCT-2003
DEFINITION BX562177 Glossina moritans moritans adult infected gut Glossina
moritans moritans cDNA clone Tse5b09.pic, mRNA sequence.
ACCESSION BX562177 GI:33372299
VERSION BX562177.1 GI:33372299
KEYWORDS EST.
SOURCE Glossina moritans moritans
ORGANISM Glossina moritans moritans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
AUTHORS 1 (bases 1 to 27)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina*
moritans moritans and expression analysis of putative immune
response genes
JOURNAL
MEDLINE
PUBMED
22881942
14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane

TITLE
Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="165h05"

Query Match
Best Local Similarity 83.3%; Score 17.6; DB 1; Length 27;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5473 TTTTTCGTAAGATATTTT 5496
|||||
1 TTTTTCGTAAGATATTTT 24

RESULT 989
AM248747 19 bp mRNA linear EST 07-JAN-2000
LOCUS 2821119.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:282119 3',
DEFINITION mRNA sequence.
ACCESSION AM248747
VERSION AM248747.1 GI:6591740
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 19)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 282119.5prime
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rmail.nih.gov
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LIML at:
www.bio.lnlnl.gov/bhrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu/LowQualitySequence>: 7 contiguous
PHRED high quality bases following vector sequence. Very low
Quality Sequence: Trace file contained 19 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LHC5 row: P column: 16
High quality sequence stop: 7.

FEATURES
source

Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:282119"
/issue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone="11b-NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAC(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match
Best Local Similarity 94.7%; Score 17.4; DB 1; Length 19;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTCGTAAGATATTTT 4482
|||||
1 TTTTTCGTAAGATATTTT 19

RESULT 990
CF291899 19 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-108.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-108, mRNA sequence.
ACCESSION CF291899
VERSION CF291899.1 GI:3360932
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-108"
/issue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone="11b-Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligotibonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 94.7%; Score 17.4; DB 1; Length 19;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTCGTAAGATATTTT 4482

Db 1 |||||
1 TGTGTTTTTTTTTTTT 19

RESULT 991

CF292072

LOCUS 19 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza

ACCESSION sativa cDNA clone 14ROOT--02-M03, mRNA sequence.
CF292072

VERSION CF292072.1 GI:33661105
KEYWORDS EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-M03"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTTTTTTTTTTT 4482
|||||
1 TGTGTTTTTTTTTTTTTT 19

Db 1 TGTGTTTTTTTTTTTTTT 19

RESULT 992

CF292144

LOCUS 19 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza

ACCESSION sativa cDNA clone 14ROOT--02-N17, mRNA sequence.
CF292144

VERSION CF292144.1 GI:33661177
KEYWORDS EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-N17"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTTTTTTTTTTT 4482
|||||
1 TGTGTTTTTTTTTTTTTT 19

Db 1 TGTGTTTTTTTTTTTTTT 19

RESULT 993

CF310688/c

LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--05-H18, mRNA sequence.
ACCESSION CF310688

VERSION CF310688.1 GI:33682449
KEYWORDS EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--05-H18"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.2%; Score 17.4; DB 1; Length 19;

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: K column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0248K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy 4466 TTTTTTTTTTTTTTTG 4484
|||||||
Db 19 TTTTTTTTTTTT 1

RESULT 997
AZ513919 19 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION 1M0360E13F Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC1M0360E13 F, genomic survey sequence.
ACCESSION AZ513919
VERSION AZ513919.1 GI:10695235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
REFERENCE
AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: B column: 13
Seq primer: CGTGTGAAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UGC1M0360E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Gy 4464 TTTTTTTTTTTTTTTT 4482
|||||||
Db 1 TTTTTTTTTTTT 1

RESULT 998
AZ645841 19 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION 1M0511G04R Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC1M0511G04 R, genomic survey sequence.
ACCESSION AZ645841
VERSION AZ645841.1 GI:11775726
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
REFERENCE
AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: G column: 04
Seq primer: CACACAGAAACGCTATGAC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

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/clone="UUCG1M0511G04"
/sex="Male"
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/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (G14732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTT 4482
Db 1 TTTTCTTTTCTTTTCTTTT 19

RESULT 999
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LOCUS
DEFINITION 1M0520N17F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
ACCESSION AZ650252
VERSION AZ650252.1 GI:11784550
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: N column: 17
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

1.19
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUCG1M0520N17"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (G14732114[gb]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTT 4482
Db 19 TTTTCTTTTCTTTTCTTTT 1

RESULT 1000
AZ654747 19 bp DNA linear GSS 14-DEC-2000
LOCUS
DEFINITION 1M0529F08F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
ACCESSION AZ654747
VERSION AZ654747.1 GI:11791893
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Isiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

OY 4464 TTTT TTTT TTTT TTTT 4482
 DB 2 TTTT TTTT TTTT TTTT 20

RESULT 1003

AZ307896 22 bp DNA linear GSS 29-SBP-2000
 LOCUS 1M0010N18F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION clone UGCG1M0010N18 F, genomic survey sequence.
 ACCESSION AZ307896
 VERSION AZ307896.1 GI:10347346
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niedermauern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0010 row: N column: 18
 Seq primer: CCGTGTAAACGACGCCACGT
 Class: plasmid ends

High quality sequence stop: 22.
 Location/Qualifiers
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

Query Match 0.2%; Score 17.4; DB 1; Length 22;
 Best Local Similarity 94.7%; Pred. No. 6.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 4463 CTTT TTTT TTTT TTTT 4481

DB 4. CTTT TTTT TTTT TTTT 22

RESULT 1004

AZ845735 22 bp DNA linear GSS 20-FBB-2001
 LOCUS 2M0145307R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION clone UGCG2M0145307 R, genomic survey sequence.
 ACCESSION AZ845735
 VERSION AZ845735.1 GI:13015643
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niedermauern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0145 row: J column: 07
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends

High quality sequence stop: 22.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0145307"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES

source

Query Match 0.2%; Score 17.4; DB 1; Length 22;
 Best Local Similarity 94.7%; Pred. No. 6.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 4470 TTTT TTTT TTTT TTTT 4488

RESULT 1007
 AZ399663 24 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0165C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0165C10 R, genomic survey sequence.
 ACCESSION AZ399663
 VERSION AZ399663.1 GI:10514737
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0165 row: C column: 10
 Seq primer: CACACAGGAAACAGCTATACC
 Claes: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0165C10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gl|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 24;
 Best Local Similarity 94.7%; Pred. No. 7.7e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 DB 6 TTTTGT TTTT TTTT TTTT G 24

RESULT 1008
 CF319499 25 bp mRNA linear EST 15-AUG-2003
 LOCUS HD-10-A10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa cDNA clone HD-10-A10, mRNA sequence.
 ACCESSION CF319499
 VERSION CF319499.1 GI:33691260
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.
 1 (bases 1 to 25)
 Kim, J.-S., Yun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C., Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE Contact: Nahm B.-H.
 JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 COMMENT Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..25
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-10-A10"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: PCR4-TOPO. Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 17.4; DB 1; Length 25;
 Best Local Similarity 94.7%; Pred. No. 8.3e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT G 19

RESULT 1009
 AU265518 26 bp mRNA linear EST 10-MAY-2002
 LOCUS AU265518 VS Dictyostelium discoideum cDNA clone VSF623 5', mRNA
 DEFINITION sequence.
 ACCESSION AU265518
 VERSION AU265518.1 GI:20524316
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 1 (bases 1 to 26)
 Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, T., Kohara, Y. and Tanaka, Y.
 Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
 Unpublished (2002)
 TITLE Contact: Hideko Urushihara
 JOURNAL Institute of Biological Sciences
 COMMENT University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

FEATURES
 source
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tshukuba.ac.jp.
 Location/Qualifiers
 1. 26
 /organism="Dictyostelium discoideum"
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 /strain="AX4"
 /db_xref="taxon:4669"
 /clone="VSP623"
 /sex="mat A"
 /dev_stage="vegetative"
 /clone_id="VS"

Query Match 0.2%; Score 17.4; DB 1; Length 26;
 Best Local Similarity 94.7%; Pred. No. 9e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4463 CTTTCTTTTCTTTTCTTTT 4481
 |||||||
 Db 8 CTCCTTTTCTTTTCTTTT 26

RESULT 1010
 AZ818035/c 26 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M008701R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0087015 R, genomic survey sequence.

ACCESSION AZ818035
 VERSION AZ818035.1 GI:12987943
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0087 row: 0 column: 15
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source

1. 26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0087015"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_id="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|g5|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.4; DB 1; Length 26;
 Best Local Similarity 94.7%; Pred. No. 9e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4462 ACTTTTCTTTTCTTTTCTTTT 4480
 |||||||
 Db 19 AATTTTCTTTTCTTTTCTTTT 1

RESULT 1011
 AZ824574/c 28 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0099D17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0099D17 F, genomic survey sequence.

ACCESSION AZ824574
 VERSION AZ824574.1 GI:12994482
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: D column: 17
 Seq primer: CTTGTATTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES
 source

1. 28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0099D17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_id="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%;	Score 17.4;	DB 1;	Length 28;
Best Local Similarity	77.8%;	Pred. No. 1e+03;		
Matches	21;	Conservative	0;	Mismatches 6;
			Indels	0;
			Gaps	0;

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Oy      4012 AAAATGAGAAAAAAGAGAGAAAAACAA 4038
          ||||| ||||| ||||| ||||| |||||
Db      27  AAAATGAGAAAAAAGAGAGAAAAACAA 1

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RESULT	1012
AZ836072/c	
LOCUS	AZ836072 28 bp DNA linear GSS 20-FEB-2001
DEFINITION	Mm13K08R Mouse 10kb plasmid UUC1M library Mms musculus genomic clone UUC2M0130K08 R, genomic survey sequence.

REFERENCE
AUTHORS
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingy, A., von
Niederhausen, A. and Wright, D. Weis, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kbp

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114[5b]AF12072.1), a copy-number inducible derivative of pAF181 [17]. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorised mouse DNA was annealed to adaptorised vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%;	Score 17.4;	DB 1;	Length 28;
Best Local Similarity	77.8%;	Pred. No. 1e+03;		
Matches 21; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0

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QY      4013 AAATGAGAAAAAGAGAGAAAACAAA 4039
          ||| | | | | | | | | | | | |
Db      28  AAAAAAAAAAAAAAAAAAAAAAA 2

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RESULT 1013		
LOCUS	CFJ28476	29 bp mRNA linear EST 18-AUG-2001
DEFINITION	NACL--03-G12. b1 Rice callus plasmid cDNA library (NACL) Oryza bativa cDNA clone NACL--03-G12, mRNA sequence.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 29)	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K., and Naim, B. H.	Large-scale Sequencing Analysis of Rice ESTs	Unpublished (2003)	Contact: Naim B. H.

```

FEATURES
source      Location/Qualifiers
1. .29

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Query Match	0.2%	Score 17.4;	DB 1;	Length 29;
Best Local Similarity	77.8%	Pred. No. 1.1e+03;		
Matches 21; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

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Qy      4012 AAAAAAGCAAAAGCAAAACAAA 4038
          ||| | ||||| | ||||| |
Db      2 AAAAAAAAAAAAAAAAAACAAA 28

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RESULT	1014
CF299716/c	
LOCUS	30 bp
CF299716	mRNA linear
DEFINITION	7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
	EST 15-AUG-2003

ACCESSION sativa cDNA clone 7LEAF--03-N11, mRNA sequence.
 VERSION CF299716
 KEYWORDS GI:33671477
 SOURCE EST.
 ORGANISM *Oryza sativa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 FEATURES
 source location/Qualifiers
 1..30
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--03-N11"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 17.4; DB 1; Length 30;
 Best Local Similarity 77.8%; Pred. No. 1.2e+03;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4013 AATGAGAAAAAGAGGAAACAAAA 4039
 Db 30 AAAAGAGAACAAAAA 4

RESULT 1015
 B0591372/c 31 bp mRNA linear EST 06-DEC-2002
 LOCUS E012712-024-017-115-T7 MP12-ADIS-024-storage root Beta vulgaris
 ACCESSION B0591372
 VERSION B0591372.1 GI:26120955
 KEYWORDS EST.
 ORGANISM *Beta vulgaris*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de

Insert Length: 31 Std Error: 0.00
 Plate: 17 row: 1 column: 15
 Seg primer: T7: GTAATGACGCTCACTATGAGGC.
 FEATURES
 source location/Qualifiers
 1..31
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:188741"
 /db_xref="taxon:161934"
 /clone="024-017-115"
 /tissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_1lb="MP12-ADIS-024-storage root"
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatuchte AG Bindeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 17.4; DB 1; Length 31;
 Best Local Similarity 77.8%; Pred. No. 1.2e+03;
 Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4013 AATGAGAAAAAGAGGAAACAAAA 4039
 Db 31 AAAAGAGAACAAAAA 5

RESULT 1016
 CF318239/c 32 bp mRNA linear EST 15-AUG-2003
 LOCUS HF--08-E17.D1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) *Oryza sativa* cDNA clone HD--08-E17, mRNA sequence.
 ACCESSION CF318239
 VERSION CF318239.1 GI:33690000
 KEYWORDS EST.
 ORGANISM *Oryza sativa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 FEATURES
 source location/Qualifiers
 1..32
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--08-E17"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_1lb="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

Db 1 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1019

LOCUS AZ45956

DEFINITION 2823002.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823002.3', mRNA sequence.

ACCESSION AM245956

VERSION AM245956.1

KEYWORDS GI:6588949

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2823002.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Berkeley MGC Sequencing project

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www.bio.lnl.gov/bbrp/image/image.html

Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector trimming: cross_match from University of Washington Genome Center

PRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu/low/QualitySequence: 9 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: trace file contained 23 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: ILNCM10 row: 0 column: 3

High quality sequence stop: 9.

Location/Qualifiers

1. .23

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2823002"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH MGC 7"

/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.28; Score 17.2; DB 1; Length 23;

Best Local Similarity 86.4%; Pred. No. 7.6e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4485

Db 1 TTTT TTTT TTTT TTTT TTTT 22

RESULT 1020

LOCUS AZ382429

DEFINITION 23 bp DNA linear GSS 02-OCT-2000

IN0139E11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0139E11 R, genomic survey sequence.

ACCESSION AZ382429

VERSION AZ382429.1

KEYWORDS GI:10496129

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE Mus musculus

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0139 row: E column: 11

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0139E11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_id="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrolitically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMP42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor-vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.28; Score 17.2; DB 1; Length 23;

Best Local Similarity 86.4%; Pred. No. 7.6e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4465 TTTT TTTT TTTT TTTT TTTT 4486

Db 23 TTTT TTTT TTTT TTTT TTTT 2

RESULT 1021

LOCUS AZ447220

DEFINITION 23 bp DNA linear GSS 04-OCT-2000

IN0244E15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244E15 F, genomic survey sequence.

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VERSION      AZ447220.1   GI:10598989
KEYWORDS
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Dunn,D., Moyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tinney,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0244 row: E column: 15
            Seq primer: CGTCTATAACGACGCCACGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES
Source       1..23
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             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUCIM0244E15"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUCIM library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male); was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pMDA2 (gi|173114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
Query Match          0.2%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred.No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4464 TTTTTTTTTTTTTTTTTTTT 4485
Db 23 TTTTTTTTTTTATTTATTTT 2
RESULT 1022
LOCUS       AU257964/c              24 bp      mRNA      linear      EST 25-APR-2002
DEFINITION  AU257964 3'-directed mouse cDNA library Mus musculus cDNA clone
ACCESSION   AU257964
VERSION     AU257964.1   GI:20330086

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KEYWORDS      EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Kato,K. and Matoba,R.
TITLE          Generation of expressed sequence tags from mouse brain
JOURNAL        Unpublished (2002)
COMMENT        Contact: Kikuya Kato
               Graduate School of Biological Sciences
               Nara Institute of Science and Technology
               8916-5 Takayama, Ikoma, Nara 630-0101, Japan
               Tel: 81-743-72-5581
               Fax: 81-743-72-5589
               Email: kkatoc@bs.aist-nara.ac.jp,
               URL:http://love2.aist-nara.ac.jp/BLD/index.html.

FEATURES
SOURCE
1..24
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0011649"
/tissue_type="brain"
/clone_lib="3"-directed mouse cDNA library"

Query Match      0.24; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      4471 TTTTCTTTTCTTCTTGACA 4492
          ||| ||||| ||||| |||||
Db      24 TTTCTATTTTCTTGACA 3

RESULT 1023
AZ307138/c
LOCUS          24 bp      DNA      GSS 29-SEP-2000
DEFINITION    IM0008G01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION     AZ307138
VERSION       AZ307138
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederharsen,A. and Wright,D. Weis,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weis
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0008 row: G column: 01
               Seq primer: CACACAGGAACACGCTTGACC
               Class: plasmid ends
               High quality sequence stop: 24.
               Location/Qualifiers
               1..24
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="CS/BL/6J"

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/db_xref="taxon:10090"
/clone="UUGC1M0008G01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5015 GAGGAGCTCTGGAGAGGAGCAGC 5036
Db 22 GAGGAGCAGAGGAGAGGAGCAGC 1

RESULT 1024
AZS14388 24 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0361H04 F, genomic survey sequence.
ACCESSION AZS14388
VERSION AZS14388.1 GI:10695704
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 04
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC1M0361H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114[gb|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4483
Db 2 AGTTCTCTTTTCTTTTCTTTTCTTTT 23

RESULT 1025
AZB14317 24 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0082C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0082C12 F, genomic survey sequence.
ACCESSION AZB14317
VERSION AZB14317.1 GI:12984321
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: C column: 12
Seq primer: CGTTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082C12"

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD29v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|g0|AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3622 GGGCTGGGCTGGAGAGAGC 3643

DB 23 GGGGGGGGGGGGGGGGGG 2

RESULT 1026

LOCUS AW247153 25 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819969.3pr:me NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2819969 3',
mRNA sequence.
ACCESSION AW247153
KEYWORDS AW247153.1 GI:6590146
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 25)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819969.5pr:me
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LIML at:
www.bio.liml.gov/bdrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu/low/QualitySequence: 7 contiguous
PHRED high quality bases following vector sequence. Vary low
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L1CM2 row: P column: 18
High quality sequence stop: 7.
Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES

source
1..25
/organism="Homo sapiens"
/mol_type="mRNA"

/db xref="taxon:9606"
/clone="IMAGE:2819969"
/issue_type="small cell carcinoma"
/cell_line="MGC3"
/lab host="NIH MGC 7"
/clone.lib="NIH MGC 7"
/note="Organ: Lung; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4467 TTTTGTGCTTGTGCTT 4488

DB 1 TTTTGTGCTTGTGCTT 22

RESULT 1027

LOCUS AZ348233/c 25 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0084G04R Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0084G04 R, genomic survey sequence.
ACCESSION AZ348233
VERSION AZ348233.1 GI:10427470
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE Dunn, D., Moyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: G column: 04
Seq primer: CACACAGAAACGCTATGACC
Clas: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0084G04"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

FEATURES

source
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0084G04"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214[gbl|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Cy 3622 GGGGTGGGGTGGAGAGAGG 3643
Db 23 GGGGTGGGGTGGGGGGGGG 2

RESULT 1028 25 bp DNA linear GSS 31-JUL-2003
CC883604
LOCUS SALK_095121.17.80.n Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_095121.17.80.n, genomic survey sequence.
ACCESSION CC883604
VERSION CC883604.1 GI:33359960
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 25)
Alonso,J.M., Lejese,T.J., Barajas,P., Chen,H., Cheuk,R., Garrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At2g45650. Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..25

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_095121.17.80.n"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 4464 TTTTGTGTGTGTGTGTGTGTGTGTGT 4485
Db 1 TTTGTGTGTGTGTGTGTGTGTGT 22

RESULT 1029 30 bp mRNA linear EST 29-MAY-2001
BG865511
LOCUS 602783643F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909811 5', mRNA sequence.
DEFINITION

ACCESSION BG865511
VERSION BG865511.1 GI:14216051
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 30)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
Plate: LLM10809 row: e column: 12
High quality sequence stop: 30.

FEATURES
source Location/Qualifiers
1..30

/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4909811"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI CGAP_SG2"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1; Nci1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

Query Match 0.2%; Score 17.2; DB 1; Length 30;
Best Local Similarity 73.3%; Pred. No. 1.2e+03; 8; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGAGAAACAAATG 4041
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAG 30

RESULT 1030

BG292912 31 bp mRNA linear EST 21-FEB-2001
LOCUS BG292912 602389549F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4501164 5', mRNA sequence.
DEFINITION

ACCESSION BG292912
VERSION BG292912.1 GI:13052227
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 31)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov

Query Match 0.2%; Score 17.2; DB 1; Length 31;
Best Local Similarity 73.3%; Pred. No. 1.2e+03; 8; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.jnl.gov
 Plate: LLM10368 row: b column: 13
 High quality sequence stop: 31.

FEATURES

source

Location/Qualifiers

1..31

/organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:4501164"
 /issue_type="retina"
 /lab_host="NIH MGC 94"
 /clone_lib="NIH MGC 94"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI,
 Site 2: SalI; cloned unidirectionally; oligo-dT primed.
 Average insert size 3.3 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH MGC library."

Query Match 0.2%; Score 17.2; DB 1; Length 31;
 Best Local Similarity 73.3%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAAATG 4041

Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 31

RESULT 1031

CF302459

LOCUS 32 bp mRNA linear EST 15-AUG-2003
 7LEAF--08-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CF302459
 CF302459

VERSION CF302459.1 GI:33674220

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm B.H.

AUTHORS

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1..32

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--08-A01"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 17.2; DB 1; Length 32;
 Best Local Similarity 73.3%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4010 CTAAATGAGAAAAAGAGAGAAACAAATG 4039

Db 3 CAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 1032

AZ579652/c

LOCUS 32 bp DNA linear GSS 13-DEC-2000
 1M0367C12R Mouse 10kb plasmid UGCGM library Mus musculus genomic

DEFINITION clone UGCGM0367C12 R, genomic survey sequence.

ACCESSION AZ579652

VERSION AZ579652.1 GI:11694081

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 32)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std. Error: 0.00

Plate: 0367 row: C column: 12

Seq primer: CACACAGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 32.

Location/Qualifiers

FEATURES

source

1..32

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0367C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.2%; Score 17.2; DB 1; Length 32;

Best Local Similarity 73.3%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAGAAACAAATG 4041
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 2

RESULT 1033

LOCUS DRI1F7S 32 bp DNA linear GSS 27-NOV-2002
DEFINITION Danio rerio genomic clone DKEX-1F7, genomic survey sequence.
ACCESSION AL735323
VERSION AL735323.1 GI:21343938
KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 32)

Humphray, S.J., Huckle, E. and Hunt, S.E.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 1F7. 1F7 is
part of the Daniokey BAC library created by R. Plasterk and N.V.
Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

1..32
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-1F7"
/cissue_type="Testis"
/note="vector pIndigoBAC-536"

Query Match 0.2%; Score 17.2; DB 1; Length 32;
Best Local Similarity 73.3%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4010 CTAATGAGAAAAAGAGAGAAACAAAA 4039
Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1034

LOCUS CF302250 34 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-J10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF-07-J10, mRNA sequence.
ACCESSION CF302250
VERSION CF302250.1 GI:33674011
KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.

1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gsbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

location/qualifiers

1..34
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiyar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-07-J10"
/cissue_type="leaf"
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/lab_host="E.coli DH10B"
/clone_1lb="rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 17.2; DB 1; Length 34;
Best Local Similarity 73.3%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4010 CTAATGAGAAAAAGAGAGAAACAAAA 4039
Db 34 CCAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1035

LOCUS BF338797 35 bp mRNA linear EST 22-NOV-2000
DEFINITION 602036229F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184167
5', mRNA sequence.
ACCESSION BF338797
VERSION BF338797.1 GI:11285216
KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens

(human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 35)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapds-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA library arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LHAM9501 row: j column: 08

High quality sequence stop: 30.

FEATURES

source

location/qualifiers

1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4184167"
/cissue_type="gliblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NCI_CGAP_Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match 0.2%; Score 17.2; DB 1; Length 35;
Best Local Similarity 73.3%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAGAAACAAATG 4041
Db 4 AAAAAAAAAAAAAAAAAAAAAAAAAAAG 33

RESULT 1036
BOS90687/c 17 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION S01717-024-018-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION
VERSION BOS90687
KEYWORDS
SOURCE Beta vulgaris
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaampiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 18 row: B column: 24
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:189432"
/db_xref="taxon:161934"
/clone="024-018-B24"
/tissue_type="storage root"
/lab_host="EMDH105"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: PCWVS-PORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzielbener SaatZucht AG Einbeck, Germany, contact: b.schultz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 17; DB 1; Length 17;
Beet Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 17 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1037
BOS91177 17 bp mRNA linear EST 06-DEC-2002
LOCUS
DEFINITION E012715-024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION
VERSION BOS91177
KEYWORDS
SOURCE Beta vulgaris

ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaampiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 17 row: B column: 22
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1..17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:188948"
/db_xref="taxon:161934"
/clone="024-017-B22"
/tissue_type="storage root"
/lab_host="EMDH105"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: PCWVS-PORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzielbener SaatZucht AG Einbeck, Germany, contact: b.schultz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 17; DB 1; Length 17;
Beet Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1038
CF290854 17 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION
VERSION CF290854
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 TITLE EST (Koehrer, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS IngoStaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
 source Location/Qualifiers
 1..18

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZ566L173"
 /tissue_type="kidney"
 /dev_stage="fetal"
 /lab_host="X1-2b1ue"
 /clone_lib="566 (synonym: hfk42)"
 /note="Vector: pMPL; Site_1: NotI; Site_2: SalI"

Query Match 0.2%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4468 TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 Db 18 TTTT TTTT TTTT TTTT G 2

RESULT 1045

CF301057 18 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION bactiva cDNA clone 7LEAF--05-M05, mRNA sequence.
 ACCESSION CF301057
 VERSION CF301057.1 GI:33672818
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..18
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--05-M05"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT T 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1046

CF301151 18 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION bactiva cDNA clone 7LEAF--05-005, mRNA sequence.
 ACCESSION CF301151
 VERSION CF301151.1 GI:33672912
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..18
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--05-005"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT T 4480
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1047

CF327587 19 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--02-C04.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION bactiva cDNA clone NACL--02-C04, mRNA sequence.
 ACCESSION CF327587
 VERSION CF327587.1 GI:33803426
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
|||||
Db 19 TTTT TTTT TTTT TTTT 3

RESULT 1050

LOCUS A2853220 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M015615F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M015615 F, genomic survey sequence.

ACCESSION A2853220
VERSION A2853220.1 GI:13041116

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Euteleostomi;
Mus. 1 (bases 1 to 19)

REFERENCE

1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss
University of Utah Genome Center

COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0156 row: J column: 15

Seq primer: CGTCTAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0156J15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
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Db 19 TTTT TTTT TTTT TTTT 3

RESULT 1051

LOCUS CE298018 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CE298018

VERSION CE298018.1 GI:33669779

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza. 1 (bases 1 to 20)

REFERENCE

1 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Noh, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

Contact: Nohm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University

JOURNAL

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 20

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--01-D19"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4468 TTTT TTTT TTTT TTTT TTTT 4484
|||||
Db 1 TTTT TTTT TTTT TTTT 17

RESULT 1052
CFJ19428
LOCUS CFJ19428 20 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-09-020.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) *Oryza sativa* cDNA clone HD-09-020, mRNA sequence.
ACCESSION CFJ19428
VERSION CFJ19428.1 GI:33691189
KEYWORDS EST.
SOURCE *Oryza sativa*
ORGANISM *Oryza sativa*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacridae; Oryzaceae; *Oryza*.
REFERENCE 1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
TITLE Contact: Nahm B.H.
COMMENT Genomic and Genetic Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-09-020"
/issue_type="Callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTT 4479
DB 1 CTTTCTTTTCTTTTCTTTT 17

RESULT 1053
AZ818055/c
LOCUS AZ818055 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M087823R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M087823 R, genomic survey sequence.
ACCESSION AZ818055
VERSION AZ818055.1 GI:12987963
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0087 row: B column: 23
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence scop: 20.
Location/Qualifiers
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M087823"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTT 4480
DB 20 TTTTCTTTTCTTTTCTTTT 4

RESULT 1054
AL048772/c
LOCUS AL048772 21 bp mRNA linear EST 04-SEP-2003
DEFINITION DKF2P566N143.r1 566 (synonym: hfxd2) Homo sapiens cDNA clone DKF2P566N143, mRNA sequence.
ACCESSION AL048772
VERSION AL048772.1 GI:4727843
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 21)
Koehler,K., Beyer,A., Mewe,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuberg, Germany.
Location/Qualifiers


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source
1. .21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ56N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone.lib="566 (synonym: hfk2)"
/notes="Vector: pAMPl; Site_1: Not; Site_2: SalI"

Query Match      0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4480
      |||||
Db 21 TTTT TTTT TTTT TTTT TTTT 5

RESULT 1055
LOCUS      A2610868      21 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION clone UUGC1M0436G12 F, genomic survey sequence.
ACCESSION  A2610868
VERSION     A2610868.1 GI:11733058
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0436 row: G column: 12
            Seq primer: CGTGTAAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
            Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
```

```
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4480
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1056
LOCUS      A2764492/c      21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION clone UUGC1M0560D04 R, genomic survey sequence.
ACCESSION  A2764492
VERSION     A2764492.1 GI:12879511
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0560 row: D column: 04
            Seq primer: CACACAGAAACAGCTATGAC
            Class: plasmid ends
            High quality sequence stop: 21.
            Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
```

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4480
|||||
Db 21 TTTT TTTT TTTT TTTT 5

RESULT 1057

LOCUS CF310806 22 bp mRNA linear EST 15-ANG-2003
DEFINITION ABF--05-K20.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-K20, mRNA sequence.

ACCESSION CF310806
VERSION CF310806.1 GI:33682567
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetic Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@pbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

location/Qualifiers
1..22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-K20"
/release_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="vector: pCR4-TOPO, Site_1: EcoRI, leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4463 CTTT TTTT TTTT TTTT TTTT 4479
|||||
Db 6 CTTT TTTT TTTT TTTT 22

RESULT 1058
AZ310057 22 bp DNA linear GSS 29-SEP-2000
LOCUS

DEFINITION 1M0018A15R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0018A15 R, genomic survey sequence.

ACCESSION AZ310057
VERSION AZ310057.1 GI:10351664
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 Row: A Column: 15
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0018A15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="vector: pMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4468 TTTT TTTT TTTT TTTT TTTT 4484
|||||
Db 1 TTTT TTTT TTTT TTTT 17

RESULT 1059
BX550903 23 bp mRNA linear EST 10-OCT-2003
LOCUS BX550903
DEFINITION BX550903 Glossina morsitans morsitans adult infected gut Glossina

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 16
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

SOURCE

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGICM0245E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGICM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1[4732114]gb[AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4464 TTTT TTTT TTTT TTTT TTTT 4480
|||||
24 TTTT TTTT TTTT TTTT TTTT 8

RESULT 1061
AU268810/c
LOCUS
DEFINITION
AU268810 25 bp mRNA linear EST 10-MAY-2002
AU268810 VS Dictyostelium discoideum cDNA clone VS1514 5', mRNA
Sequence.
AU268810
AU268810.1 GI:20527608
EST.
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
1 (bases 1 to 25)
Urushihara, H., Morio, T., Saito, T., Koriiki, E., Ochiai, H., Maeda, M.,
Takenuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664

JOURNAL
COMMENT

FEATURES
source
Fax: 81-298-53-6614
Email: hideko@biol.taukuba.ac.jp.
Location/Qualifiers

1. 25
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="V51514"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="V5"

Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4468 TTTTGTCTTGTCTTGA 4492
|||||
Db 25 TTTTGTCTTGTCTTGA 1

RESULT 1062
AM245275 25 bp mRNA linear EST 07-JUN-2000
LOCUS 2819996.3prlme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819996 3',
DEFINITION mRNA sequence.
ACCESSION AM245275
VERSION AM245275.1 GI:6568268
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTs: 2819996.5prlme
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Lung
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequences: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequences: Trace file contained 25 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L10C3 row: A column: 21.

FEATURES

source

1. 25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819996"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Size: 1. XhoI; Site: 2;
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by lung Hong in

the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 4466 TTTTGTCTTGTCTTGA 4490
|||||
Db 1 TTTTGTCTTGTCTTGA 25

RESULT 1063
BI094828 25 bp mRNA linear EST 14-DEC-2001
LOCUS EST-CD34N-028 cDNA library of human CD 34+ stem/progenitor cells
DEFINITION Homo sapiens cDNA 3', mRNA sequence.
ACCESSION BI094828
VERSION BI094828.1 GI:17737205
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 25)
Zhou, G., Chen, J., Lee, S., Terry, C., Rowley, J.D. and Wang, S.M.
The pattern of gene expression in human hematopoietic CD34+
stem/progenitor cells
Unpublished (2001)
Contact: Wang SM
Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
Email: swangl@midway.uchicago.edu
This EST fragment was amplified from cDNA library of human CD 34+
stem/progenitor cells with Glgi technique (Generation of Longer
cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
the first CATG site of the target cDNA sequence.
Seq primer: M3 Forward

FEATURES

source

1. 25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Bone marrow"
/cell_type="CD34+ stem/progenitor cells"
/clone_lib="cDNA library of human CD 34+ stem/progenitor
cells"
/note="ESTs converted from the SAGE tag sequences using
GLGI method"

Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4472 TTTTGTCTTGTCTTGA 4496
|||||
Db 1 TTTTGTCTTGTCTTGA 25

RESULT 1064
CF300714 25 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--05-E19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION bativa cDNA clone 7LEAF--05-E19, mRNA sequence.
ACCESSION CF300714
VERSION CF300714.1 GI:33672475
KEYWORDS EST.
SOURCE Oryza sativa

10.5 kb range using preparative agarose gel

Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTT 4488
|||||
Db TTTTCTTTTCTTTTCTTATT 2

RESULT 1070
A2828616/c 26 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0105007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0105007 R, genomic survey sequence.
ACCESSION A2828616
VERSION A2828616.1 GI:12998524
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Relliy, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weisse, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: 0 column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0105007"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/shares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF19072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptorized vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source

Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4450 TGGGTGCATGACCTTTTCTT 4474
|||||
Db TGGCTGCATGACCTTTTCTTCT 1

RESULT 1071
AA852828/c 28 bp mRNA linear EST 20-JUN-2002
LOCUS
DEFINITION NHTBCae16e07f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA
clone NHTBCae16e07, mRNA sequence.
ACCESSION AA852828
VERSION AA852828.1 GI:2941421
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 28)
Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G.,
Beckstrom-Steinberg, S.M., Green, E.D., Powell, J.I., Yang, L.M.,
Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.
SCAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
Contact: Libin Jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
Seq primer: M13 Forward.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTBCae16e07"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/clone_1lb="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site 1. EORI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)"

FEATURES
source

Query Match 0.2%; Score 17; DB 1; Length 28;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4015 ATGAGAAAAAGAGAGAAAAA 4039
|||||
Db ACGAGAAAAA 2

RESULT 1072
DR31A15T 30 bp DNA linear GSS 22-NOV-2002
LOCUS
DEFINITION Danio rerio genomic clone DKRY-31A15, genomic survey sequence.
ACCESSION AL987581
VERSION AL987581.1 GI:25176586
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 30)
Humphray, S.J., Huckle, E. and Hunt, S.E.

FEATURES
AUTHORS

TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Camps, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hummer@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 31A15. 31A15 is part of the Dadokey BAC Library created by R. Plasterik and N.V. Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rexio/.

FEATURES

Location/Qualifiers
1..30

/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-31A15"
/issue_type="Testis"
/note="vector pindigobAC-536"

Query Match 0.2%; Score 17; DB 1; Length 30;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACA 4037
|||||
5 AAAAAGAAAAAAGAAAAA 30

RESULT 1073

AM245279 31 bp mRNA linear EST 07-JAN-2000
LOCUS 2820044.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2820044.3',
DEFINITION mRNA sequence.

ACCESSION AM245279
VERSION AM245279.1 GI:6588272
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
1 (bases 1 to 31)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)

Other ESTs: 2820044.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bnrl/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PhRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very low
Quality Sequence: Trace file contained 31 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this CDNA insert was polyadenylated.
Plate: LNCM3 row: C column: 21.

FEATURES

Location/Qualifiers
1..31

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820044"
/issue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:

ECORI; CDNA made by oligo-dT priming. Directionally
cloned into EcorI/XhoI sites using the following 5'
adaptor: GGACGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 17; DB 1; Length 31;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACA 4039
|||||
31 AAAAAGAAAAAAGAAAAA 4

RESULT 1074

BG531309 34 bp mRNA linear EST 03-APR-2001
LOCUS 602559543F1 NIH_MGC_61 Homo sapiens CDNA clone IMAGE:4697459.5',
DEFINITION mRNA sequence.

ACCESSION BG531309
VERSION BG531309.1 GI:13522846
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
1 (bases 1 to 34)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)

Other ESTs: 602559543F1
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: LNCM1526 row: e column: 12
High quality sequence stop: 34.
Location/Qualifiers
1..34

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4697459"
/issue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NIH_MGC_61"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctggcc); Site_2: SfiI (ggccttggcc);
Double-stranded CDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dT(30)BN-3'
(where B = A, C, G or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

Query Match 0.2%; Score 17; DB 1; Length 34;
Best Local Similarity 69.7%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4007 GGTCTAAATGAGAAAAAGAGAAAAACA 4039
|||||
2 CGGAGAAAAAAGAAAAAAGAAAAA 34

Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTCTCT 4483
 |||||
 Db 1 TTTTCTTTTCTTCTCT 20

RESULT 1078
 CF336815 20 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid CDNA
 DEFINITION library (JMT) Oryza sativa CDNA clone JMT--07-A04, mRNA sequence.
 ACCESSION CF336815
 VERSION CF336815.1 GI:33822012
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomic and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--07-A04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

FEATURES
 source

Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4468 TTTTCTTTTCTTCTCT 4487
 |||||
 Db 1 TTTTCTTTTCTTCTCT 20

RESULT 1079
 AZ343730 20 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ343730
 DEFINITION 1M0077820F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0077820 F, genomic survey sequence.
 ACCESSION AZ343730
 VERSION AZ343730.1 GI:10422288
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0077 row: E column: 20
 Seq primer: CGTGTAAACGACGCCAGCT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0077E20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114[gbl]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTCTCT 4483
 |||||
 Db 1 TTTTCTTTTCTTCTCT 20

RESULT 1080
 AZ346143 20 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ346143/c
 DEFINITION 1M008191F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M008191 F, genomic survey sequence.
 ACCESSION AZ346143
 VERSION AZ346143.1 GI:10425380
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isaiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: P column: 11
Seq primer: CGTTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. 20

FEATURES

SOURCE

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0081P11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained From the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of pLambda RI+. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2% Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 4469 TTTTTTTTTTGGTCCTT 4488
||||||| |||||
20 TCTTTTCTTGTCCTT 1

Db 20 TCTTTTCTTGTCCTT 1

RESULT 1081

AZ633741/c

LOCUS AZ633741 20 bp DNA linear GSS 13-DEC-20000

DEFINITION 1M0489G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0489G12 F, genomic survey sequence.

ACCESSION AZ633741

VERSION AZ633741.1 GI:11755931

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE	Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Relly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nedderhausen,A. and Wright,D.,Weiss,R.		
JOURNAL	Unpublished (2000)		
COMMENT	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
	Contact: Robert B. Weiss		
	University of Utah		
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA		
	Tel: 801 585 5606		
	Fax: 801 585 7177		
	Email: ddum@genetics.utah.edu		
	Insert Length: 10000 Std Error: 0.00		
	Size: 0489 row: G column: 12		
	Seq primer: CGTGTAAACGACGCCACGT		
	Class: plasmid ends		
	High quality sequence stop: 20.		
FEATURES	Location/Qualifiers		
source	1..20		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="UGCIM0489G12"		
	/sex="Male"		
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"		
	/clone_id="Mouse 10kb plasmid UGCIM library"		
	/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource		
	(http://www.jax.org/resources/documents/dnares/). The DNA was hydromedically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gii4732114[bp AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Qy	4464	TTTTTTTTTTTTTTTTTT	4483
Db	20	TTTGCTTTTTTTTTTTTT	1
RESULT 1082			
LOCUS	AM248782	21 bp	mRNA
DEFINITION	2821017.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821017 3', mRNA sequence.	linear	EST 07-JAN-2000
ACCESSION	AM248782		
VERSION	AM248782.1	GI:6591775	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 21)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)		

**JOURNAL
COMMENT**

Unpublished (1999)
Other ESTs: 2821017.5p.tme
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-1@mail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (ULNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/ULNL at:
www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from university of Washington Genome Center
PHRAP suite. Poly-T Identification: patchmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 21
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a Ahoi site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LCM5 row: L column: 10
High quality sequence stop: 21.
Location/Qualifiers
1..21

Query Match	0.2%	Score 16.8	DB 1	Length 21
Best Local Similarity	90.0%	Pred. No. 7.3e+02		
Matches 18; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
Oy	4464	TTTTTTTTTTTTTTTTTTTT	4483	
db	1	TTTTTTTTTAAATTTTTTT	20	

RESULT	1083
LOCUS	CF319122
DEFINITION	CF319122 21 bp mRNA linear EST 15-AUG-2003
ACCESSION	HD--09-107.g1 OsHDAct1-overexpressing transgenic rice plasmid cDNA library (HD)
VERSION	CF319122
KEYWORDS	CF319122.1 GI:33690883
SOURCE	EST.
ORGANISM	Oryza sativa
	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, U.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.
	Genomics and Genetics Institute, Greengene Biotech Inc., Division of Biotechnology and Bioinformatics, Myoungi University
	Yongin, Kyeonggi, Korea

FEATURES
source

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahe@gbio.com, bhnahebio.myongji.ac.kr
Location/Qualifiers
1. 21

Query Match	0.2%	Score 16.8	DB 1	Length 21
Best Local Similarity	90.0%	Pred. No. 7.3e+02		
Matches 18; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0
QY	4466	TTTTTTTTTTTTTTTTTCT	4465	
	1	TTTTTTTTTTTTTTTCGT	20	

RESULT 1084
CF319625/c

LOCUS
DEFINITION
CF319625 21 bp mRNA linear EST 15-AUG-2003
HD-10-D06.g1 O6HDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD-10-D06, mRNA sequence.
CF319625
CF319625.1 GI:33691366
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 21)
Kim,U.S., Yun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Yonsei University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@gbio.com, bhnaahm@bio.myonsei.ac.kr.
Location/Qualifiers

FEATURES
source
1..21

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FEATURES
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        location/Qualifiers
            1..21
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                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="HD-10-D06"
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                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
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                /clone_id="OSHDAc1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
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                derived from rice Histone Deacetylase overexpression
                line."
    
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Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 21 TTTT TTTT TTTT TTTT ATAG 2

RESULT 1085
AZ468862 21 bp DNA linear GSS 04-OCT-2000
LOCUS IM0282004F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0282004 F, genomic survey sequence.
ACCESSION AZ468862
VERSION AZ468862.1 GI:10626987
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0282 row: 0 column: 04
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/clone="UGCM0282004"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.2%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3613 TTGGGGAATGGGGTGGGGGT 3632
|||||
Db 1 TTGGGGGGTGGGGTGGGGGT 20

RESULT 1086
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LOCUS IM0412D23F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0412D23 F, genomic survey sequence.
ACCESSION AZ597932
VERSION AZ597932.1 GI:11720122
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0412 row: D column: 23
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0412D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTT 4483
 |||||
 Db 1 TTTTCTTTTCTTTT 20

RESULT 1087

AZ647578

LOCUS AZ647578 21 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0514117F Mouse 10kb plasmid UGCM library Mus musculus genomic

ACCESSION AZ647578
 clone UGCM0514117 F, genomic survey sequence.

VERSION AZ647578.1 GI:11779183

KEYWORDS

SOURCE GSS.
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0514 row: 1 column: 17
 Seq primer: CCGTGTAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0514117"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /note="Vector: pMD42uv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI:4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 7.3e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTT 4483
 |||||
 Db 1 TTTTCTTTTCTTTT 20

RESULT 1088

AM246884

LOCUS AM246884 22 bp mRNA linear EST 07-JUN-2000
 DEFINITION 2822626.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822626 3',

ACCESSION AM246884
 mRNA sequence.

VERSION AM246884.1 GI:6589877

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Other ESTs: 2822626.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: DCTP/DTF cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/bnpr/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross_match from University of Washington Genome Center
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 20
 contiguous PHRED high quality bases following vector sequence. Very
 Low Quality Sequence: Trace file contained 22 contiguous distinct
 peaks following vector sequence.
 Plate: L1CM9 row: 0 column: 11
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

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 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GCGACGAC(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. No. 8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCT 4482
 |||||
 Db 1 CTTTCTTTTCTTTTCT 20

RESULT 1089

AZ345485

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 DEFINITION IM0080C02F Mouse 10kb plasmid UGCM library Mus musculus genomic

ACCESSION AZ345485
 VERSION AZ345485.1 GI:10424722
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhanssen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Seq primer: CGTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 22.
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 /strain="C57BL/6J"
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 /clone="UUGC1M0080C02"
 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. No. 8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4463 CTTTTTTTTTTTTTTTTT 4482
 |||||
 Db 3 CTTTTTTTTTAATTTTTT 22

RESULT 1090
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 LOCUS 1M0542D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION
 clone UUGC1M0542D04 F, genomic survey sequence.

ACCESSION AZ662734
 VERSION AZ662734.1 GI:11799880
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhanssen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0542 row: D column: 04
 Seq primer: CGTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 23.
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC1M0542D04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 8.e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4466 TTTTTTTTTTTTTTTTGT 4485
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 Db 23 TTTTTTTTTTAATTAAGT 4

RESULT 1091
 CF331867
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 DEFINITION NACL--08-C13.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--08-C13, mRNA sequence.

VERSION CF331867.1 GI:33811957
 KEYWORDS EST.
 SOURCE *Oryza sativa*
 ORGANISM *Oryza sativa*
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; *Oryza*.
 1 (bases 1 to 24)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.U., Lee,T.H., Shin,Y.C.,
 Authors Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Title Large-scale Sequencing Analysis of Rice ESTs
 Journal Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.
 FEATURES
 Location/Qualifiers

```

1..24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACT--08-C13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACT)"
/note="vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.2%	Score 16.8;	DB 1;	Length 24;
Best Local Similarity	90.0%;	Pred. No.9.5e+02;		
Matches 18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

Qy	4467	TTTTTTTTTTTTTTTTTTGTC	4486
Db	1	TTTTTTTTTTTTTTTTTTACTC	20

RESULT 1092					
CF331868/c					
LOCUS	CF331868	24 bp	mRNA	linear	EST 18-AUG-2003
DEFINITION	NACL--08-C13.g1 Rice callus plasmid cDNA library (NACL) Oryza				
ACCESSION	saliva cDNA clone NACL--08-C13, mRNA sequence.				
	CF331868				

SOURCE ORGANISM	PHYLOGENETIC POSITION
<i>Oryza sativa</i>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; <i>Oryza</i> .

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 24)	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.	Large-scale Sequencing Analysis of Rice ESTs	unpublished (2003)	Contact: Nahm B. H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```
FEATURES
source
location/Qualifiers
1. .24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/clote=Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 16.0; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. NO. 9.Se+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      24 TTTTTTTTTTTTACTC 5

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Query Match      0.2%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4467 TTTTTTTTTTTTTTGGTC 4486
          |||||
Db       24 TTTTTTTTTTTTTTACTC 5

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RESULT 1093
AZ782507
LOCUS

LOCUS	24 bp	DNA	linear
LOCUS	AZ782527		GS5 16-FEB-2001
DEFINITION	MZ00222L22R	Mouse 10kb	plasmid ucgcgm library Mus musculus genomic
DEFINITION	clone ucgc2m00222L22 R,	genomic	survey sequence.

ACCESSION	A2782507	
VERSION	A2782507.1	GI:12916299
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE	AUTHORS
1 (bases 1 to 24)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Fax: 801 585 7177
Email: ddum@genetics.utah.edu

```

Inhibc denglin: 10000 500 Error: 0.00
Plate: 0022 row: L column: 22
Seq primer: CACACAGGAAACAGCTATGACC

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Class: plasmid ends
High quality sequence stop: 24.
location/offsets

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Source
1. .24
/organism="Mus musculus"
/-f "mus_musculus.fasta"
/
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/strain="C57BL/6J"
/db_xref="taxon:10090"

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```

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

```

musculus C57BL/6J (male) was obtained from the Jackson
/notes=Vector: PWD42nv; Purified genomic DNA from M.
/clone_ids=mouse 10KD plasmid uocum library".

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to

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electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XH10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4466 TTTTCTTTCTTTCTTTGT 4485
Db 4 TTTTCTTTCTTTCTTTGT 23

RESULT 1094
D19580/c

DEFINITION D19580 25 bp mRNA linear EST 12-DEC-1995
MUSGS00987 Mouse 3'-directed Mus musculus domesticus cDNA clone
mb1686 3', mRNA sequence.

ACCESSION D19580 GI:1089438
VERSION D19580
KEYWORDS EST.
SOURCE Mus musculus domesticus (western European house mouse)
ORGANISM Mus musculus domesticus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K.

TITLE Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
JOURNAL Unpublished (1995)
COMMENT Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and
Matsubara, K.

FEATURES
source
Location/Qualifiers
3-1 Yamada-oka, Suita, Osaka 565, Japan.
1..25

/organism="Mus musculus domesticus"
/mol_type="mRNA"
/strain="C57BL/6J"
/sub_species="domesticus"
/db_xref="taxon:10092"
/clone="mb1686"
/issue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_lib="Mouse 3'-directed"

Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4466 TTTTCTTTCTTTCTTTGT 4485
Db 25 TTTCTTTCTTTCTTTGT 6

RESULT 1095
CF282351/c
LOCUS CF282351 28 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.

ACCESSION CF282351 GI:33659738
VERSION CF282351
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrtaroidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 28)
AUTHORS Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.-H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..28

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-N05"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAAAAA 4039
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1096
CF321885/c

LOCUS CF321885 28 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-13-E16.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD-13-E16, mRNA sequence.

ACCESSION CF321885
VERSION CF321885
KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrtaroidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 28)
AUTHORS Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.-H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..28

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-13-E16"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E. coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid"

cdna library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with Aha(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAA 4039
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1097
CF330748/c 28 bp mRNA linear EST 18-AUG-2003
LOCUS CF330748
DEFINITION sativa cDNA clone NACL--06-014, mRNA sequence.
ACCESSION CF330748 GI:33809717
VERSION CF330748.1
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Rharioideae; Oryzaceae; Oryza.
1 (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source 1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-014"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAA 4039
Db 28 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1098
CF330938 28 bp mRNA linear EST 18-AUG-2003
LOCUS CF330938
DEFINITION NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF330938
VERSION CF330938.1 GI:33810102
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Rharioideae; Oryzaceae; Oryza.
1 (bases 1 to 28)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

Query Match 0.2%; Score 16.8; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1099
AZ399637/c 28 bp DNA linear GSS 03-OCT-2000
LOCUS AZ399637
DEFINITION IM0165N04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION AZ399637
VERSION AZ399637.1 GI:10514711
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: down@genetics.utah.edu
Insert Length: 10000
Plate: 0165
row: N
col: 04
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends

Journal
COMMENT

<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD242 [g1473211|gb|AF129072.1], a copy-number inducible derivative of plasmid λ . The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

High quality sequence stop: 28.

<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [g14732114(gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorised mouse DNA was annealed to adaptorised vector DNA, and transformed into chemically-competent *E. coli* XL10-GOLD (Stratagene) cells and selected for ampicillin resistance."

High quality sequence atop: 28
 Clabs: plasmid ends

FEATURES

source

1..28

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0286K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039
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Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1102

AZ493138 28 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0327F02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0327F02 R, genomic survey sequence.
ACCESSION AZ493138
VERSION AZ493138.1 GI:1066355
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0327 row: F column: 02
Seq primer: CACACAGAAACGCTATAC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers 1..28

FEATURES
source

source

1..28

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0327F02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1103

AZ653365 28 bp DNA linear GSS 14-DEC-2000
LOCUS 1M05227E02P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M05227E02 F, genomic survey sequence.
ACCESSION AZ653365
VERSION AZ653365.1 GI:11790511
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0527 row: E column: 02
Seq primer: CGTTTAAACACGCGCACT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers 1..28

FEATURES
source

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/sex="Male"
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/clone_1b="Mouse 10kb plasmid UUCGCM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214|g1473214|g1473214|g1473214), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.24; Score 16.8; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1104
AZ785035/c 28 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0628J01R Mouse 10kb plasmid UUCGCM library Mus musculus genomic
ACCESSION
AZ785035
VERSION
AZ785035.1 GI:12921373
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: J column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
SOURCE
1. .28
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0028J01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UUCGCM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1473214|g1473214|g1473214|g1473214), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match 0.24; Score 16.8; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1105
AZ824519/c 28 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0609109F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
ACCESSION
AZ824519
VERSION
AZ824519.1 GI:12994427
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: I column: 09
Seq primer: CGTGTGAAAAGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
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/strain="C57BL/6J"

/sex="Male"
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 /clone.lib="Mouse 10kb plasmid UUCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 28;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1108

LOCUS TA291A010 28 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 291a01, reverse sequence,
 genomic survey sequence.

ACCESSION AL486613
 VERSION AL486613.1 GI:11853602

KEYWORDS GSS.
 SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
 1..28
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 /db_xref="taxon:5691"
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Query Match 0.2%; Score 16.8; DB 1; Length 28;
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 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1109

LOCUS TA379D11P/c 28 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 379d11, forward sequence,
 genomic survey sequence.

ACCESSION AL497637
 VERSION AL497637.1 GI:11873359

KEYWORDS GSS.
 SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 28)
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
 1..28
 /organism="Trypanosoma brucei"
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Query Match 0.2%; Score 16.8; DB 1; Length 28;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1110

LOCUS TA29A09P/c 28 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 29a09, forward sequence,
 genomic survey sequence.

ACCESSION AL453073
 VERSION AL453073.1 GI:11854584

KEYWORDS GSS.
 SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 28)
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

TITLE
JOURNAL

Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission

COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1998).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source

1.28
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/db_xref="taxon:5691"
/clone="29a09"

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Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAAA 4039
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1111
CF279536/c

LOCUS 14ETL--05-N22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa cDNA clone 14ETL--05-N22, mRNA sequence.
ACCESSION CF279536
VERSION CF279536.1 GI:33656922
KEYWORDS EST.

SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 29)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1.29
/organism="Oryza sativa"
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/culturivar="Nackdong"
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(14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAAA 4039
DB 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1112
CF299920

LOCUS 7LEAF--04-C02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--04-C02, mRNA sequence.
ACCESSION CF299920
VERSION CF299920.1 GI:33671681
KEYWORDS EST.

SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 29)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1.29
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAAA 4039
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1113
CF312601

LOCUS 29 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-G22, mRNA sequence.
ACCESSION CF312601
VERSION CF312601.1 GI:33684362
KEYWORDS EST.

SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eubartoideae; Oryzaceae; Oryza.
1 (bases 1 to 29)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
location/Qualifiers
1..29
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="ABF-08-G22"
/rlesue_type="leaf"
/dev_sstage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match
Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1114
A2389566 29 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0150D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC1M0150D21 F, genomic survey sequence.
ACCESSION A2389566
VERSION A2389566.1 GI:10503274
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 21
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends

FEATURES
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location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|g2|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1115
A2414283 29 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0186G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC1M0186G12 R, genomic survey sequence.
ACCESSION A2414283
VERSION A2414283.1 GI:10538296
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0188 row: G column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES
source

1. 29
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M018612"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1117
LOCUS A2451930 29 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0251E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION A2451930
VERSION A2451930.1 GI:10608203
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: E column: 05
Seq primer: CACACAGAAACAGCTATCAGC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

FEATURES

Location/Qualifiers

source

1. 29
Location/Qualifiers
/organism="Mus musculus"
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 0.2%; Score 16.8; DB 1; Length 29;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1117
LOCUS A2468402 29 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0281G24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION A2468402
VERSION A2468402.1 GI:10626527
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: G column: 24
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

FEATURES

Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0281G24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGCAAAACAAA 4039
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1118
AZ466793/c 29 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0315N21F Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION clone UGC1M0315N21 F, genomic survey sequence.
ACCESSION AZ466793
VERSION A2486793
KEYWORDS GSS.1 GI:10653915
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: N column: 21
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
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/clone="UGC1M0315N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGCAAAACAAA 4039
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1119
AZ661709/c 29 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0540K20F Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION clone UGC1M0540K20 F, genomic survey sequence.
ACCESSION AZ661709
VERSION A2661709
KEYWORDS GSS.1 GI:11798855
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0540 row: K column: 20
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

FEATURES
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/organism="Mus musculus"
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/sex="Male"
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAGAGAGAAACAAA 4039
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1120

A2784208

LOCUS A2784208 29 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0026113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0026113 R, genomic survey sequence.

ACCESSION

A2784208

VERSION A2784208.1 GI:12919703

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: 1 column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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/organism="Mus musculus"
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/strain="C57BL/6J"

FEATURES

SOURCE

1. 29

/organism="Mus musculus"

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/strain="C57BL/6J"

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/clone="UUGC2M0026113"
/sex="Male"
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/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAGAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1121

A2806470

LOCUS A2806470 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0068102 R, genomic survey sequence.

ACCESSION

A2806470

VERSION A2806470.1 GI:12969849

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: 1 column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"

FEATURES

SOURCE

1. 29

/organism="Mus musculus"

/mol_type="genomic DNA"

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/clone="UUGC2M0068102"
/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1122

AZ812242 29 bp DNA linear GSS 20-FEB-2001

LOCUS 2M007BJ1SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC2M007BJ1S R, genomic survey sequence.

ACCESSION AZ812242

VERSION AZ812242.1 GI:12981296

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: J column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES

Source 1..29
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M007BJ1S"

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/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1123

AZ868731 29 bp DNA linear GSS 21-FEB-2001

LOCUS 2M0180L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC2M0180L02 R, genomic survey sequence.

ACCESSION AZ868731

VERSION AZ868731.1 GI:13072338

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: L column: 02
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180L02"
/sex="Male"

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039
 Db 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1126
 BG666435
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 DEFINITION DRRCRC02 Rat DRG Library Rattus norvegicus cDNA clone DRRCRC02 5',
 mRNA sequence.
 ACCESSION BG666435
 VERSION BG666435.1 GI:13888357
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 Rattus.
 1 (bases 1 to 30)
 XIAO,H.S., HUANG,Q.H., ZHANG,P.X., BAO,L., LU,Y.J., GUO,C.,
 YANG,L., HUANG,W.J., FU,G., XU,S.H., CHENG,X.P., YAN,Q., ZHU,Z.D.,
 ZHANG,X., CHEN,Z., HAN,Z.G. and ZHANG,X.
 Identification of gene expression profile of dorsal root ganglion
 in the rat peripheral axotomy model of neuropathic pain
 Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
 22056133
 MEDLINE
 PUBMED 12060780
 COMMENT Contact: Zhang Xu
 Laboratory of Sensory System
 Institute of Neuroscience
 320 Yue Yang Road, Shanghai 200031, P.R.China
 Tel: 86-21-64748700-121
 Fax: 86-21-64713446
 Email: xu.zhang@ion.ac.cn
 This clone is also available at Chinese National Human Genome
 Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
 Pudong New Area, P.R.China. Please contact with Zhang Xu
 (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
 PCR primers
 FORWARD: T3
 BACKWARD: T7
 Seq primer: T3
 POLYA=No.

FEATURES
 Source location/Qualifiers
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 /clone="DRRCRC02"
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 /tissue_type="dorsal root ganglion"
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Query Match 0.2%; Score 16.8; DB 1; Length 30;
 Best Local Similarity 75.0%; Pred.No.1.4e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1127
 CF280699/c
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 CF280699
 ACCESSION CF280699.1 GI:33658085
 VERSION

30 bp mRNA linear EST 14-AUG-2003
 14FTL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14FTL)
 CF280699
 ACCESSION CF280699.1 GI:33658085
 VERSION

KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarthroideae; Oryzaceae; Oryza.
 1 (bases 1 to 30)
 KIM,J.S., JUN,K.M., CHEONG,P.J., KIM,M.J., LEE,T.H., SHIN,Y.C.,
 SONG,S.I., KIM,J.K., KIM,Y.-K. and NAM,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nam B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..30
 /organism="Oryza sativa"
 /mol_type="mRNA"
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 /db_xref="taxon:4530"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E. coli DH10B"
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 (14FTL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

FEATURES
 Source location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="Nackdong"

Query Match 0.2%; Score 16.8; DB 1; Length 30;
 Best Local Similarity 75.0%; Pred.No.1.4e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039
 Db 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1128
 CF292086
 LOCUS
 DEFINITION 14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-M10, mRNA sequence.
 ACCESSION CF292086
 VERSION CF292086.1 GI:33661119
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarthroideae; Oryzaceae; Oryza.
 1 (bases 1 to 30)
 KIM,J.S., JUN,K.M., CHEONG,P.J., KIM,M.J., LEE,T.H., SHIN,Y.C.,
 SONG,S.I., KIM,J.K., KIM,Y.-K. and NAM,B.H.
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 Unpublished (2003)
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..30
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"

FEATURES
 Source location/Qualifiers
 1..30
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 /mol_type="mRNA"
 /cultivar="Nackdong"

/db_xref="taxon:4530"
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Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAGAGAGAAACAAA 4039
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1129

CF299555/c

LOCUS CF299555 30 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CF299555
VERSION CF299555.1 GI:33671316

KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..30
Location/Qualifiers

/organism="Oryza sativa"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAGAGAGAAACAAA 4039
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1130

CF312417/c

LOCUS CF312417 30 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--08-C19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--08-C19, mRNA sequence.

ACCESSION CF312417
VERSION CF312417.1 GI:33684178

KEYWORDS EST..gag
SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..30
Location/Qualifiers

/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--08-C19"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAGAGAGAAACAAA 4039
1 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1131

CF322226/c

LOCUS CF322226 30 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--13-M02.b1 OSHDACL-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--13-M02, mRNA sequence.

ACCESSION CF322226
VERSION CF322226.1 GI:33693987

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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source
1..30
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD--13-M02"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAATGAGAAAAAGAGAAACAAA 4039
Db 30 AAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1132
LOCUS CF327835 30 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF327835
VERSION CF327835.1 GI:33803920
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..30
/organism="Oryza sativa"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAATGAGAAAAAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAA 28

TITLE JOURNAL
COMMENT

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RESULT 1133
LOCUS CF336555/c 30 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-K13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--06-K13, mRNA sequence.
ACCESSION CF336555
VERSION CF336555.1 GI:33821487
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..30
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAATGAGAAAAAGAGAAACAAA 4039
Db 30 AAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1134
LOCUS AZ357603/c 30 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0099H17F Mouse 10kb plasmid tUGCIM library Mus musculus genomic
clone tUGCIM0099H17 F, genomic survey sequence.
ACCESSION AZ357603
VERSION AZ357603.1 GI:10471303
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
TITLE JOURNAL
COMMENT

```

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: H column: 17
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES

SOURCE

Location/Qualifiers
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/mol_type="genomic DNA"
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/clone="UUCG1M0099H17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAAATGAGAAAAAGAGAAAAA 4039
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1135

AZ443322

30 bp DNA linear GSS 04-OCT-2000

DEFINITION 1M0237120R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0237120 R, genomic survey sequence.

ACCESSION

AZ443322

VERSION

AZ443322.1 GI:10591190

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermauser, A. and Wright, D., Weiss, R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

COMMENT

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0237 row: L column: 20
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Class: plasmid ends
High quality sequence stop: 30.

FEATURES

SOURCE

Location/Qualifiers
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/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4012 AAAATGAGAAAAAGAGAAAAA 4039
|||||
Db 3 AAAAAAAAAAAAAAAAAAAAAA 30

RESULT 1136

AZ455741

30 bp DNA linear GSS 04-OCT-2000

DEFINITION 1M0258D16F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0258D16 F, genomic survey sequence.

ACCESSION

AZ455741

VERSION

AZ455741.1 GI:10613866

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermauser, A. and Wright, D., Weiss, R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: D column: 16
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Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

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/clone_lib="Mouse 10kb plasmid UGCM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1137
AZ481739/c 30 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0306N12F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM1M0306N12 F, genomic survey sequence.
ACCESSION AZ481739
VERSION AZ481739.1 GI:10642804
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: A column: 12
Seq primer: CGTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
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/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAAAACAAA 4039
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1138
AZ582114/c 30 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0374J17F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM1M0374J17 F, genomic survey sequence.
ACCESSION AZ582114
VERSION AZ582114.1 GI:11700674
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0374 row: J column: 17
Seq primer: CGTGTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES

source

1.30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M0374017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|47321419|gb|AF128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1139
AW249485/c 31 bp mRNA linear EST 07-JAN-2000
LOCUS AW249485
DEFINITION 2821429.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821429 3',
mRNA sequence.
ACCESSION AW249485
VERSION AW249485.1 GI:6592478
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 31)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821429.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTP/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality

FEATURES

source

Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 20
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: Trace file contained 31 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNC6 row: M column: 14
High quality sequence stop: 20.
Location/Qualifiers

1.31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821429"
/issue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH MGC 7"
/note="Organ: lung; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1140
BX569502/c 31 bp mRNA linear EST 14-OCT-2003
LOCUS BX569502
DEFINITION BX569502 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse9a03_jic, mRNA sequence.
ACCESSION BX569502
VERSION BX569502.1 GI:33437420
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 31)
Lehane, M.D., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Donald, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22861942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2NW

All clones with suffix g1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from the 3' end.

FEATURES

source

Location/Qualifiers

1..31
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse9a03.plc"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1141

LOCUS

CF278807

DEFINITION

14ETL--04-N15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION

CF278807

VERSION

CF278807.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 31)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..31

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--04-N15"

/issue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 31;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1142

LOCUS

CF300345/c

DEFINITION

7LEAF--04-L08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION

CF300345

VERSION

CF300345.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 31)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..31

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--04-L08"

/issue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 31;

Best Local Similarity 75.0%; Pred. No. 1.4e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAAA 4039

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1143

LOCUS

AZ333315/c

DEFINITION

1M062A21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0062A21 F, genomic survey sequence.

ACCESSION

AZ333315

VERSION

AZ333315.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 31)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: A column: 21
Seq primer: CGTGTGTAACGACGCGCATGCT
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0062A21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAA 4039
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1144

AZ375973 31 bp DNA linear GSS 02-OCT-2000
LOCUS AZ375973
DEFINITION 1M0129D08R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0129D08 R, genomic survey sequence.
ACCESSION AZ375973
VERSION AZ375973.1 GI:10489673
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: D column: 08
Seq primer: CACACGAAACAGCATGAC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES

source

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1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0129D08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD42N; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1145

AZ510092 31 bp DNA linear GSS 05-OCT-2000
LOCUS AZ510092
DEFINITION 1M0354P14F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0354P14 F, genomic survey sequence.
ACCESSION AZ510092
VERSION AZ510092.1 GI:10691408
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0354 row: P column: 14
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers

FEATURES

source

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1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16.8; DB 1; Length 31;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1146
 A2623538 31 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0461G21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0461G21 F, genomic survey sequence.
 ACCESSION A2623538
 VERSION A2623538.1 GI:11745728
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0461 row: G column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers

FEATURES

source

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1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0461G21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.2%; Score 16.8; DB 1; Length 31;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAAA 4039
 Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1147
 A2627692 31 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0469C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0469C09 R, genomic survey sequence.
 ACCESSION A2627692
 VERSION A2627692.1 GI:11749882
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0469 row: C column: 09
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers

FEATURES

source

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 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UUGC2M014002"
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 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 75.0%; Pred. No. 1.4e+03; Length 31;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1148

A2778697 31 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0014002F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0014002 F, genomic survey sequence.
 ACCESSION A2778697
 VERSION A2778697.1 GI:12908605
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0014 row: O column: 02
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 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers

FEATURES

source

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 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 75.0%; Pred. No. 1.4e+03; Length 31;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1149

A2821215 31 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0093F21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0093F21 R, genomic survey sequence.
 ACCESSION A2821215
 VERSION A2821215.1 GI:12991123
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0093 row: F column: 21
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Dy 4012 AAATGAGAAAAAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1150
AZ826618 31 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0102C19F Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0102C19 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: C column: 19

Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES
SOURCE

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/clone="UGCM0102C19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Dy 4012 AAATGAGAAAAAGAGAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1151
AZ486763/c 31 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION 1M0315A11F Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM1M0315A11 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: A column: 11
Seq primer: CGTTGTAAAACGACGGCAGT

Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES

source

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/note="Vector: PMD42v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAAAA 4039
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1152

AM327277

LOCUS AM327277 32 bp mRNA linear EST 28-JAN-2000
DEFINITION dg01d07.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:284628 5', mRNA sequence.

ACCESSION AM327277

VERSION AM327277.1 GI:6797772

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Edge Biosystems

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Plate: LICM0028 row: G column: 13

Seq primer: -21M13 forward primer (ABI).

Location/Qualifiers

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/clone="IMAGE:284628"
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/clone_1ib="NIH MGC_2"
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1153

CF291773/c

LOCUS CF291773 32 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-F12, mRNA sequence.

ACCESSION CF291773

VERSION CF291773.1 GI:3360806

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.

1 (bases 1 to 32)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, U.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..32

Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-F12"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E. coli DH10B"

/clone_1ib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAAAA 4039
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1154

CF299386/c

LOCUS CF299386 32 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-G07, mRNA sequence.

ACCESSION CF299386

VERSION CF299386.1 GI:33671147

KEYWORDS EST.

SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 32) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnah@ggbio.com, bhnah@bio.myongji.ac.kr.
FEATURES	location/Qualifiers
SOURCE	1..32 /organism="Oryza sativa" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:4530" /clone="7LEAF--03-G07" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_11b="Rice leaf plasmid cDNA library II (7LEAF)" /note="vector: pCR4-TOPO; site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match	0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity	75.0%; Pred. No. 1.5e+03;
Matches	21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy	4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
Db	32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 1155	
CF309233	
LOCUS	CF309233 32 bp mRNA linear EST 15-AUG-2003
DEFINITION	ABF--03-F14.G1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-F14, mRNA sequence.
ACCESSION	CF309233
VERSION	CF309233.1 GI:33680994
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 32) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnah@ggbio.com, bhnah@bio.myongji.ac.kr.
FEATURES	location/Qualifiers
SOURCE	1..32 /organism="Oryza sativa" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:4530" /clone="ABF--03-F14"

[illegible]

CF313717/c 32 bp mRNA linear EST 15-AUG-2003
 LOCUS HD-01-P05.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa cDNA clone HD-01-P05, mRNA sequence.
 ACCESSION CF313717
 VERSION CF313717.1 GI:33685478
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-01-P05"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
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 cDNA library (HD)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
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 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1158
 CF321046/c 32 bp mRNA linear EST 15-AUG-2003
 LOCUS HD-12-C15.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa cDNA clone HD-12-C15, mRNA sequence.
 ACCESSION CF321046
 VERSION CF321046.1 GI:33692807
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..32
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
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 /tissue_type="callus"
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 /lab_host="E.coli DH10B"
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TITLE JOURNAL
 COMMENT

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..32
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-12-C15"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
 |||||
 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1159
 CF328471/c 32 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--03-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION NACL--03-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza
 ACCESSION CF328471
 VERSION CF328471.1 GI:33805189
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /clone="NACL--03-G09"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TITLE JOURNAL
 COMMENT

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
 ||||| ||||| ||||| ||||| |||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1160
 CF331270 32 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--07-F08.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--07-F08, mRNA sequence.
 ACCESSION CF331270
 VERSION CF331270.1 GI:33810751
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.,
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
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 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--07-F08"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
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 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1161
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 LOCUS AZ459536/c
 DEFINITION 1M0264M16F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0264M16 F, genomic survey sequence.
 ACCESSION AZ459536
 VERSION AZ459536.1 GI:10617577
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 32)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0264 row: M column: 16
 Seq primer: GCTTGTAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers
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 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
 ||||| ||||| ||||| ||||| |||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1162
 AZ470832 32 bp DNA linear GSS 04-OCT-2000
 LOCUS AZ470832
 DEFINITION 1M0285F14F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0285F14 F, genomic survey sequence.
 ACCESSION AZ470832
 VERSION AZ470832.1 GI:10628957
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 32)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellily,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: F column: 14
Seq primer: CCGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 32.

FEATURES

source

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/strain="C57BL/6J"
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/clone="UUCGCM0285F14"
/sex="Male"
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/clone_1ib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAA 4039

DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1163

A2611890/c

LOCUS 32 bp DNA linear GSS 13-DEC-2000

DEFINITION 1M0438E02R Mouse 10kb plasmid UUCGCM library Mus musculus genomic

ACCESSION A2611890

VERSION A2611890.1 GI:11734080

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: E column: 02
Seq primer: CACACAGAAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES

source

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/clone_1ib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAAA 4039

DB 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1164

A2778018

LOCUS 32 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0012020R Mouse 10kb plasmid UUCGCM library Mus musculus genomic

ACCESSION A2778018

VERSION A2778018.1 GI:12907220

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0012 row: 0 column: 20
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

source

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/notice="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1165

DR85L21T 32 bp DNA linear GSS 22-NOV-2002
 LOCUS DR85L21T 32 bp DNA linear GSS 22-NOV-2002
 DEFINITION Dantio rerio genomic clone DKEX-85L21, genomic survey sequence.
 ACCESSION AL986044
 VERSION AL986044.1 GI:25187956
 KEYWORDS GSS

SOURCE Dantio rerio (zebrafish)
 ORGANISM Dantio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Dantio.
 1 (bases 1 to 32)

REFERENCE Humphray, S.J., Huckle, E. and Hunt, S.E.
 TITLE Direct Submission
 JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphrey@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 85L21. 85L21 is part of the Dantiokey BAC library created by R. Plastek and N.V. Keygene.
 Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

Location/Qualifiers
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/organism="Dantio rerio"
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/db_xref="taxon:7955"
/clone="DKEX-85L21"
/issue_type="Testis"
/notice="vector pindigoBAC-536"

Query Match 0.2%; Score 16.8; DB 1; Length 32;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAACAAA 4039
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1166

CF334899/c

LOCUS CF334899/c 33 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--04-F19_g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--04-F19, mRNA sequence.
 ACCESSION CF334899
 VERSION CF334899.1 GI:33818141
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 33)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

TITLE

JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--04-F19"
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/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notice="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis thaliana Carboxyl methyltransferase overexpression line."

Query Match 0.2%; Score 16.8; DB 1; Length 33;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAACAAA 4039
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 1167

BU431798/c

LOCUS BU431798 33 bp mRNA linear EST 09-SEP-2002
 DEFINITION 601655890R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855694 3',

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ACCESSION      BU431798
VERSION        BU431798.1
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 33)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapb-remail.nih.gov
                Tissue Procurement: DCTD/DTF
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: L1CM570 row: c column: 23
                High quality sequence stop: 31.
FEATURES       Location/Qualifiers
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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH-MGC_66"
                /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.8 kb. Library constructed by Life
                Technologies."
Oy            4012 AAAATGAGAAAAAGAGGAAACAAA 4039
Db            32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

Query Match      0.2%; Score 16.8; DB 1; Length 33;
Beet Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 1168
CF291613/c
LOCUS         CF291613          33 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION   14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-B21, mRNA sequence.
ACCESSION    CF291613
VERSION      CF291613.1
KEYWORDS     GI:33660646
SOURCE       EST.
ORGANISM     Oryza sativa
              Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 33)
AUTHORS       Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc., Division
              of Bioscience and Bioinformatics, Yonsei University
              Yongsin, Kyoeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
              Location/Qualifiers
              1..33
FEATURES
SOURCE

```

[illegible]

```

RESULT 1170
CF326967/c      33 bp      mRNA      linear      EST 18-AUG-2003
LOCUS
DEFINITION      NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION      CF326967
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-E04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 1171
CF328313      33 bp      mRNA      linear      EST 18-AUG-2003
LOCUS
DEFINITION      NACL--03-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION      CF328313
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
location/Qualifiers
1..33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-C14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_1lb="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1172
CF336752/c      33 bp      mRNA      linear      EST 18-AUG-2003
LOCUS
DEFINITION      JMT--06-019.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--06-019, mRNA sequence.
ACCESSION      CF336752
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
location/Qualifiers
1..33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--06-019"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
pared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGACAAACAAA 4039

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Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT	1173				
CF337105/c					
LOCUS	CF337105	33 bp	mRNA	linear	EST 18-AUG-2003
DEFINITION	UMT--07-G18.b1 AtUMT-overexpressing transgenic rice plasmid cDNA				
ACCESSION	CF337105				
VERSION	CF337105.1	GI:33822596			
KEYWORDS	EST.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				

FEATURES	Location/Qualifiers
source	1. .33

RESULT	1174
AZ486795/c	
LOCUS	33 bp DNA linear GSS 05-OCT-2000
DEFINITION	Mus musculus genomic clone UUCGCM03J15P22 F, genomic survey sequence.
ACCESSION	AZ486795
VERSION	AZ486795.1 GI:10653918
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
KARYOTE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 33)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,K., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mus whole genome scaffolding with paired end reads from 10kb

JOURNAL
COMMENT
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

FEATURES	Location/Qualifiers
source	1. .33

RESULT	1175
AZ627839/c	
LOCUS	33 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM0474B02 Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0474B02 F, genomic survey sequence.
ACCESSION	AZ627839
VERSION	AZ627839
KEYWORDS	AZ627839.1 GI:11750125
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)
TITLE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ismail,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,K. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 02
Seq primer: CGTTGTAACGACGCGCCACT
Class: plasmid ends
High quality sequence stop: 33.

Location/Qualifiers
1. .33

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U081M04.4B02"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: pMD24nv. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (G11473211[g]A123072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.2%	Score 16.8	DB 1	Length 33
Best Local Similarity	75.0%	Pred. No. 1.5e+03		
Matches 21	Conservative	0	Mismatches 7	Indels 0
				Gaps 0

Qy	4012	AAAA	TGAG	AAAA	AAAG	GAG	AAAA	CAAAA	4039
Db	33	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAAAAA	AAAAA	AAAAA	6	

RESULT	1176				
DR41A4T					
LOCUS	DR41A4T	34 bp	DNA	linear	GSS 22-NOV-2002
DEFINITION	Danio rerio genomic clone	DXEY-41A4,	genomic	sequence.	
ACCESSION	AL280969				
VERSION	AL280969.1	GI:25182658			
KEYWORDS	GSS.				
SOURCE	Danio rerio				
ORGANISM	Danio rerio (zebrafish)				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE
AUTHORS
I (bases 1 to 34)
Humphray, S.J., Huckle, E. and Hunt, S.E.

TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished

COMMENT
This sequence was generated from the T7 end of BAC 41A4. 41A4 is part of the Dariokey BAC Library created by R. Plasterk and N.V.

FEATURES

```

/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKFZ-41A4"
/tissue_type="Testis"
/note="Vector pindigobAC-536"

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Query Match	0.2%	Score 16.8	DB 1	Length 34
Best Local Similarity	75.0%	Pred. No. 1.6e+03		
Matches 21; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

Oy	4012	AAATGAGAAAAAGAGAGAAAA	CAAAA	4039
Db	6	AAAAAACAAAAA	AAAAA	33

RESULT 1177	
LOCUS	AU267170/c
DEFINITION	AU267170 23 bp mRNA linear EST 10-MAY-2002 AU267170 VS Dictyostelium discoideum cDNA clone VSH259 5', mRNA sequence.
ACCESSION	AU267170
VERSION	AU267170
KEYWORDS	AU267170.1 GI:20525968
SOURCE	EST.
ORGANISM	Dictyostelium discoideum
	Dictyostelium discoideum

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota: Mycetozoa: Dictyostelidae: Dictyoselium. 1 (Passes 1 to 23)	Uneshihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Nee,da, Y.	Takeuchi, I., Kohara, Y. and Tanaka, Y.	Population analyses of cdnas from unicellular and multicellular stages of Dictyoselium discoidium	Unpublished (2002)
	Contact: Hideko Uneshihara			

Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba,
Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES	Location/Qualifiers
source	1. .23

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organism="Dicycostellum discoideum"
/mol_type="MRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH269"
/sex="mat A"
/dev_stage="vegetative"
/clone_id="VS"

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Query Match	0.2%	Score 16.6;	DB 1;	Length 23;
Best Local Similarity	82.6%	Pred. No. 9.4e+02;		
Matches 19;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy	4465	TTTTTTTTTTTTTTTTTGTCT	4
Db	23	TTTTTTTTTTATTTCTATTGTTT	1

LOCUS	DEFINITION	EST
CE300172	23 bp mRNA linear	15-AUG-2003
CE300172	7EAF-04-H15.b1 Rice leaf plasmid cDNA library II (7EAF) Oryza sativa cDNA clone 7EAF-04-H15, mRNA sequence.	

ACCESSION	CP300172
VERSION	CP300172.1
KEYWORDS	EST.
SOURCE	Oryza sativa

ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 23)
TITLE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Jun,K.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL	Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES	location/Qualifiers
SOURCE	1..23
	/organism="Oryza sativa"
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	/culivar="Nackdong"
	/db_xref="taxon:4530"
	/clone="7LEAF--04-H15"
	/tissue type="leaf"
	/dev stage="7 days after germination"
	/lab_host="E.coli DH10B"
	/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
	/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match	0.2%; Score 16.6; DB 1; Length 23;
Best Local Similarity	82.6%; Pred.No.9.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Ok	4465 TTTTCTTTTTTTTTTTGCT 4487
Db	1 TTTTCTTTTTTTTAATTATTT 23
RESULT 1179	
LOCUS	CF302134 23 bp mRNA linear EST 15-AUG-2003
DEFINITION	7LEAF--07-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION	sativa cDNA clone 7LEAF--07-F21, mRNA sequence.
VERSION	CF302134
KEYWORDS	CF302134.1 GI:3673895
SOURCE	EST.
ORGANISM	Oryza sativa
REFERENCE	Oryza sativa
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
TITLE	1 (bases 1 to 23)
JOURNAL	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Jun,K.K., Kim,Y.-K. and Nahm,B.H.
COMMENT	large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES	Location/Qualifiers
SOURCE	1..23
	/organism="Oryza sativa"
	/mol_type="rRNA"
	/culivar="Nackdong"
	/db_xref="taxon:4530"
	/clone="7LEAF--07-F21"
	/tissue type="leaf"

Query Match	0.23	Score 16.6	DB 1	Length 23
Best Local Similarity	82.6%	Pred. No. 9.4e+02		
Matches 19	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Qy	4466	TTTTTTTTTTTTTTTGTCTT	4468	
Db	1	TTTTTTTTTTTTTCTACTCT	23	
RESULT 1180				
AZ374746				
LOCUS	AZ374746	23 bp	DNA	linear
DEFINITION	IM0127D1SR Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127D1S R, genomic survey sequence.			
ACCESSION	AZ374746			
VERSION	AZ374746.1	GI:1048446		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0127 row: D column: 15 Seq primer: CACACAGGAAACACGCTATGCAC Clas: plasmid ends High quality sequence stop: 23. Location/Qualifiers 1. 23 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0127D1S" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (g1473214 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated			

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3616 GGGATGGGCTGGGCTGGGCA 3638
Db 1 GTGGCTGGGCTGGGCTGGGCA 23

RESULT 1181

AZ469557 23 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION IM0283A09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0283A09 F, genomic survey sequence.

ACCESSION AZ469557
VERSION AZ469557.1 GI:10627682
KEYWORDS
SOURCE GSS.

ORGANISM Mus musculus (house mouse)
MUS musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0283 row: A column: 09
Seq primer: CCTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0283A09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[g]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5310 TTTGTCTCTCTCTCTCTCTC 5332
Db 1 TTTGTCTCTCTCTCTCTCTC 23

RESULT 1182

AV740046/c 25 bp mRNA linear EST 17-OCT-2000
LOCUS
DEFINITION AV740046 CB Homo sapiens cDNA clone CBFAWFO4.5', mRNA sequence.

ACCESSION AV740046
VERSION AV740046.1 GI:10857627
KEYWORDS
SOURCE EST.

ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 25)
Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z., Chen, S., Mao, M. and Chen, Z.

REFERENCE
AUTHORS Homo sapiens CB library cDNA clones
Unpublished (2000)
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-jin Hospital
157 Rui-jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mshl@ms.sh.cn
This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

TITLE
JOURNAL
COMMENT
Location/Qualifiers

FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFAWFO4"
/cissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4467 TTTTGTCTCTCTCTCTCTGAG 4491
Db 25 TTTTGTCTCTCTCTCTCTG 1

RESULT 1183

BG925523/c 25 bp mRNA linear EST 06-NOV-2001
LOCUS
DEFINITION HNC5-1-D5.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG925523
VERSION BG925523.1 GI:14320046
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 25)
 AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sachdev, G., Mui, P., Agarwal, P., Badger, A.M., Lee, D.C., Gowen, M. and Laik, M.W.
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritis cartilage cDNA libraries
 JOURNAL Osteoarthritis Cartilage 9 (7), 641-653 (2001)
 MEDLINE 21482651
 PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UM2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay_kumar-1@sk.com
 Seq primer: T7.
 FEATURES
 source location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cvs_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2869 AGGAGGAGGAGGTGGGTAGG 2891
 Db 23 AGGAGGAGGAGGAGGGAAGG 1

RESULT 1184
 CF297950 25 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--01-C05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sative cDNA clone 7LEAF--01-C05, mRNA sequence.
 ACCESSION CF297950
 VERSION CF297950.1 GI:33667711
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 25)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..25
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cvs_type="Nackdong"
 /db_xref="taxon:4530"
 /clone_lib="7LEAF--01-C05"
 /cvs_type="leaf"
 /dev_stage="7 days after germination"

REFERENCE 1 (bases 1 to 25)
 AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sachdev, G., Mui, P., Agarwal, P., Badger, A.M., Lee, D.C., Gowen, M. and Laik, M.W.
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritis cartilage cDNA libraries
 JOURNAL Osteoarthritis Cartilage 9 (7), 641-653 (2001)
 MEDLINE 21482651
 PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UM2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay_kumar-1@sk.com
 Seq primer: T7.
 FEATURES
 source location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cvs_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6467 TTTTTCCTGTTTGATATAG 6489
 Db 1 TTTTTCCTGTTTGATATAG 23

RESULT 1185
 AZ340193 25 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0072J03F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION clone UGCG1M0072J03 F, genomic survey sequence.
 ACCESSION AZ340193
 VERSION AZ340193.1 GI:10415397
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0072 row: J column: 03
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence strop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="UGCG1M0072J03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6953 GAAGGAGGGAGGAGATGAC 6975
Db 24 GGAAGGAGGAGGAGGAGGAGG 2

RESULT 1186

LOCUS AZ510562/c 25 bp DNA linear GSS 05-OCT-2000
DEFINITION M0355F11F Mouse 10kb plasmid UGCG1M library Mus musculus genomic clone UGCG1M0355F11 F, genomic survey sequence.

ACCESSION AZ510562
VERSION AZ510562.1 GI:10691878
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0355 row: F column: 11
Seq primer: CGTGTAAACGACGCGCAGT
Clases: plasmid ends
High quality sequence stop: 25.

Location/Qualifiers

FEATURES 1. .25
SOURCE /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0355F11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3615 GGGGAATGGGTGGGTGGAG 3637
Db 23 GGGGAAGGGGGGGGGGGGGG 1

RESULT 1187

LOCUS AL048684 30 bp mRNA linear EST 04-SEP-2003
DEFINITION DKEZ566C043_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKEZ566C043, mRNA sequence.

ACCESSION AL048684
VERSION AL048684.1 GI:4727755
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 30)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

JOURNAL Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.
Contact: MIPS
MIPS

TITLE Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

FEATURES 1. .30
SOURCE /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEZ566C043"
/issue_type="Kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1lb="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.2%; Score 16.6; DB 1; Length 30;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4017 GAGAAAAAGAGAGAAACAAA 4039
Db 8 GAGAAAAAGAGAGAGAGAGAGAG 30

RESULT 1188

LOCUS AL048732 30 bp mRNA linear EST 04-SEP-2003
DEFINITION DKEZ566I053_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKEZ566I053, mRNA sequence.

ACCESSION AL048732
VERSION AL048732.1 GI:4727803
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 30)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

JOURNAL Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.
Contact: MIPS
MIPS

TITLE Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

```

source
1..30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ5661053"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="xyl-2blune"
/clone_lib="566 (synonym: hfkd2)"
/note="vector: pAMP1; Site_1: NotI; site_2: SalI"

Query Match      0.2%; Score 16.6; DB 1; Length 30;
Best Local Similarity 82.6%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      4017 GAGAAAAAAGAGACAAAACA 4039
Db      8 GAGAAAAAAAAAAAAAAAAAAAAA 30
|||||
|||||

RESULT 1189
R59306/c
LOCUS       R59306               32 bp     mRNA          linear   EST 24-MAY-1995
DEFINITION  yihc10.b1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE       J3793.3, similar to gb:M29064 HETEROGENEOUS NUCLEAR
RIBONUCLEOPROTEINS A2/B1 (HUMAN);, mRNA sequence.
ACCESSION   R59306
VERSION     R59306.1 GI:830001
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 32)
Hillier,L., Clark,N., Dubchak,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Watson,R., Williamson,A., Woldmann,P. and
Wilson,R.
The Mashu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNLN
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: SP6
High quality sequence stop: 1.
Location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:J37903"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="MDH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: lafmid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5';
AACGGAGAATTGCAGCGCAGCAATTTTCTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the lafmid BA vector.
```

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Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

Query Match          0.2%; Score 16.6; DB 1; Length 32;
Best Local Similarity 71.0%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Cy 4009 TCTAAATGAGAAAAAGAGAAAAACAAA 4039
|||||
31 TCTAAGGAGAAAAAAGAAAAA 1

RESULT 1190
CF328492/c 34 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--03-G22.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G22, mRNA sequence.
ACCESSION CF328492
VERSION CF328492.1 GI:33805230
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifere
1. .34
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-G22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E. coli DH10B"
/clone_1ib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source

Query Match          0.2%; Score 16.6; DB 1; Length 34;
Best Local Similarity 71.0%; Pred. No. 1.7e+03;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Cy 4004 TTAGGTCTAAATGAGAAAAAGAGAAAA 4034
|||||
31 TCATGCTATAAAAAAAGAAAAA 1

RESULT 1191
BM658677 18 bp mRNA linear EST 27-FEB-2002
LOCUS BM658677
DEFINITION L2V602766363.R1 CSRQFLX37 pig adrenal Sus scrofa cDNA, mRNA
sequence.
ACCESSION BM658677
VERSION BM658677.1 GI:18958948
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

```


REFERENCE 1 (bases 1 to 18)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Porcine ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.

FEATURES
source Location/Qualifiers
1.18
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/clone_id="CSEQFL37 pig adrenal"
/note="Organ: adrenal gland; Vector: pBluescript SK+;
Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GCGAATTCGAGCTCCACCGCGGTCGCGCGCGCTGAG. Sequence 3' of
the inserts (AAGATTCGATATCAAGCTTATCGATACCGTCGACCTGAG.
non-normalized library, sequenced 3' with M13R primer."

Query Match 0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTCTTTCTTTCTTT 4481
|||||
Db 1 TTTTCTTTCTTTCTTTCTTT 18

RESULT 1192
CF300456 18 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--04-N23, mRNA sequence.
ACCESSION CF300456.1 GI:33672217
VERSION EST.
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1.18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source Location/Qualifiers
1.18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTCTTTCTTTCTTT 4481
|||||
Db 1 TTTTCTTTCTTTCTTTCTTT 18

RESULT 1193
CF302409 18 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--07-N19, mRNA sequence.
ACCESSION CF302409.1 GI:33674170
VERSION EST.
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1.18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-N19"
/tissue_type="leaf"
/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source Location/Qualifiers
1.18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-N19"
/tissue_type="leaf"
/dev stage="7 days after germination"
/lab host="E.coli DH10B"
/clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 6e+02; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4467 TTTTCTTTCTTTCTTTCTTT 4484
|||||
Db 1 TTTTCTTTCTTTCTTTCTTT 18

RESULT 1194
CF320046 18 bp mRNA linear EST 15-AUG-2003
LOCUS HD-10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD-10-M11, mRNA sequence.
ACCESSION CF320046.1 GI:33691807
VERSION EST.
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.
1 (bases 1 to 18)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
TITLE Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. 18
 Location/Qualifiers

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-10-M11"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDACI-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match
 Best Local Similarity 94.4%; Pred. No. 6e+02; Length 19;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4481
 |||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1195
CF329137/c
LOCUS CF329137 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-P15-g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329137
VERSION CF329137.1 GI:33806511
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
 source
 1. 19
 Location/Qualifiers

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--04-P15"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match
 Best Local Similarity 94.4%; Pred. No. 6.8e+02; Length 19;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4471 TTTT TTTT TTTT TTTT TTTT 4488
 |||||
Db 19 TTTT TTTT TTTT TTTT TTTT 2

RESULT 1196
CF334610
LOCUS CF334610 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--03-P13.b1 ACUMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-P13, mRNA sequence.
ACCESSION CF334610
VERSION CF334610.1 GI:33817556
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
 source
 1. 19
 Location/Qualifiers

/organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--03-P13"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ACUMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match
 Best Local Similarity 94.4%; Pred. No. 6.8e+02; Length 19;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4481
 |||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1197
A2360314/c
LOCUS A2360314 19 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0103G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0103G03 R, genomic survey sequence.
ACCESSION A2360314
VERSION A2360314.1 GI:10474014
KEYWORDS GSS.

ORGANISM	Mus musculus
REFERENCE	Bakaygora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
AUTHORS	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0560 row: L column: 07 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGCLM0560L07" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_idb="Mouse 10kb plasmid UGCIM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydromyemically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gil4732114 pb AF129072.1], a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
FEATURES	
SOURCE	
Query Match	0.2%; Score 16.4; DB 1; Length 19;
Best Local Similarity	94.4%; Pred. No. 6.8e+02;
Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	4462 ACTTTTCTTTTTTTTTTTT 4479
Db	18 AAATTTTCTTTTTTTTTT 1
RESULT 1199	
LOCUS	CF293087
DEFINITION	30DG5--02-C07.g1 Rice leaf plasmid cDNA library I (30DG5) Oryza sativa cDNA clone 30DG5--02-C07, mRNA sequence.
ACCESSION	CF293087
VERSION	CF293087.1 GI:33662120
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa

ORGANISM	Mus musculus
REFERENCE	Bakayocet; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
AUTHORS	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0560 row: L column: 07 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGCM0560L07" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lid="Mouse 10kb plasmid UGCM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydromyemically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gil4732114 pb AF129072.1], a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
FEATURES	
SOURCE	
Query Match	0.2%; Score 16.4; DB 1; Length 19;
Best Local Similarity	94.4%; Pred. No. 6.8e+02;
Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Oy	4462 ACTTTTCTTTTTTTTTTTT 4479
Db	18 AAATTTTCTTTTTTTTTT 1
RESULT 1199	
LOCUS	CF293087 21 bp mRNA linear EST 14-AUG-2003
DEFINITION	30DG5--02-C07.g1 Rice leaf plasmid cDNA library 1 (30DG5) Oryza
ACCESSION	CF293087
VERSION	CF293087.1 GI:33662120
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa

REFERENCE 1 (bases 1 to 21)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source
 1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
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 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DS)"
 /notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match
 Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4469 TTTT TTTT TTTT TTTT TTTT GTC 4486
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 1 TTTT TTTT TTTT TTTT TTTT GAC 18

RESULT 1200
 LOCUS CF309614 21 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.
 ACCESSION CF309614
 VERSION CF309614.1 GI:33681375
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 21)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source
 1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"

/lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
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 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match
 Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4461 GACTTT TTTT TTTT TTTT TTTT TTTT 4478
 |||||
 1 GGCTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 1201
 LOCUS AZ316361/c 22 bp DNA linear GSS 29-SEP-2000
 DEFINITION IM0034116F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0034116 F, genomic survey sequence.
 ACCESSION AZ316361
 VERSION AZ316361.1 GI:10364110
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0034 row: 1 column: 16
 Seq primer: CGTGTGAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES
 source

1..22
 /organism="Mus musculus"
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 /strain="C57BL/6J"
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 /clone="UGCG1M0034116"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

pMD22 (g1473311[gb]APR29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%	Score 16.4	DB 1	Length 22
Best Local Similarity	94.4%	Pred. No. 9.3e+02		
Matches 17	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

[illegible]

RESULT 1202
AZ854229

LOCUS	AZ8543229	22 bp	DNA	linear	GSS 21-FEB-2001	genomic
DEFINITION	2M0157C14R Mouse 10kb plasmid UGCG1M library Mus musculus genomic clone UUGC2M0157C14 R, genomic survey sequence.					

ACCESSION	AZ854229
VERSION	AZ854229.1
KEYWORDS	GI:13043139
SOURCE	GSS.
PROJECT	Mass sequencing (house mouse)

SOURCE	MUS MUSCULUS (HOUSE MOUSE)
ORGANISM	MUS MUSCULUS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE	1 (bases 1 to 22)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE	Author	Year	Journal	Volume	Issue	Page(s)	DOI	PMID
Mouse whole genome scaffolding with paired end reads from 10kbp								

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES

```

1. 22
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0157C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1fb="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PMD249; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative of
PMD242 (g114732114|g1b|AR29072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.2%	Score 16.4;	DB 1;	Length 22;
Best Local Similarity	94.4%;	Pred. No. 9.3e+02;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	4022	AAAAGAGAGAAACAAA	4039
Db	1	AAAAGAGAGAAACAAA	18

RESULT 1203
AL587602

LOCUS	AL587602	23 DP	mRNA	linear	EST U2-PW-200
DEFINITION	AL587602 BP Chicken Brain Library				
	ROS052PF08, mRNA sequence.				

ACCESSION	AL587602
VERSION	AL587602.1
KEYWORDS	GI:13192636
COMMENT	EST.
	Callus culture (chicken)

SOURCE	ORGANISM	GALLUS gallus	(chicken)
	Gallus gallus		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauiria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE 1 Phasianinae; Gallus, (barns 1 to 23)

AUTHORS	Murray, F.
TITLE	BP Chicken Brain Library

JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray

Roblin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200

GCGGGCCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
(*6854-)

FEATURES

SOURCE

```

Location/Qualifiers
1..23
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059P08"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1, Site 1: Not1, Site 2: SalI, Cloned
unirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TGACCTCGAG 3' ; 3' adaptor sequence: 5'
GGGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
Clontech (#6854-1)"

```

ACCESSION CP293725 GI:33661758
 VERSION EST.
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoae; Oryza.
 1 (bases 1 to 24)
 Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..24
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DS-01-K12"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DS)"
 /note="Vector: PCR4-TOP0, Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16.4; DB 1; Length 24;
 Best Local Similarity 94.4%; Pred. No. 1.1e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTCTTG 4484
 |||||
 1 TTTTCTTTTCTTTTCTTG 18

RESULT 1205
 LOCUS A1000095/c 25 bp mRNA linear EST 27-AUG-1998
 DEFINITION os61a08.g1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1609814 3' similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST; contains L1.b1 MSRI repetitive element;; mRNA sequence.
 ACCESSION A1000095
 VERSION A1000095.1 GI:3190649
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 25)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-rt@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1953 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from AmerSham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1609814"
 /sex="female, pooled"
 /tissue_type="breast"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Br2"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. This library is the normalized version of NCI CGAP Br1.1. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2417 ACACCAACATCACCACC 2434
 |||||
 22 ACACCAACACACCCACC 5

RESULT 1206
 LOCUS A2764498/c 25 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0560K04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0560K04 R, genomic survey sequence.
 ACCESSION A2764498
 VERSION A2764498.1 GI:12879523
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: K column: 04
 Seq primer: CACACGAGAACGCTAGACG
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0560K04"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTT 4479
 |||||
 Db 18 AATTTTCTTTTCTTTT 1

RESULT 1207

AZ764502 26 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0560U03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0560U03 R, genomic survey sequence.

ACCESSION AZ764502
 VERSION AZ764502.1 GI:12879531.

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: L column: 03
 Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source Location/Qualifiers
 1..26

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0560U03"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.4; DB 1; Length 26;
 Best Local Similarity 76.9%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4021 AAAAGAGAGAAACAAATGTTATT 4046
 |||||
 Db 1 AAAAAAAAAAAAAAAAAATTTT 26

RESULT 1208

AZ818035 26 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0087O15R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0087O15 R, genomic survey sequence.

ACCESSION AZ818035
 VERSION AZ818035.1 GI:12987943

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0087 row: O column: 15
 Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source Location/Qualifiers
 1..26

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0087O15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_11b="Mouse 10kb plasmid UNGCM library"
/note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.4; DB 1; Length 26;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4023 AAGAGAGAAAACAAATGTTATTTT 4048

Db 1 AAAAAAAAAAAAAAAAAATTTTTTTT 26

RESULT 1209
LOCUS N89936 27 bp mRNA linear EST 02-APR-1996
DEFINITION Zb2e12.81 Soares fetal lung NBHL19W Homo sapiens CDNA clone
IMAGE:302926.3 similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,
MITOCHONDRIAL PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION N89936 GI:1443263

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 27)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, B., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: eselw@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: RT primer

FEATURES
High quality sequence stop: 8.

Location/Qualifiers

1..27

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1247858"

/db_xref="taxon:9606"

/clone="IMAGE:302926"

/dev_stage="19 weeks"

/lab_host="PH10B (ampicillin resistant)"

/clone_11b="Soares fetal lung NBHL19W"

/note="Organ: lung; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GTTACCAATCTGAGACGAGCGCCGACATTTTTTTTTTTT-3']
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Felina Bonaldi. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."

Query Match 0.2%; Score 16.4; DB 1; Length 27;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4014 AATGAGAAAAAGAGAGAAAACAAA 4039

Db 27 AATGCAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1210

LOCUS TA257B07P 27 bp DNA linear GSS 13-DEC-2000

DEFINITION T. Brucei sheared genomic DNA clone 257b07, forward sequence.

ACCESSION AL483278

VERSION AL483278.1 GI:11849602

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 27)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..27

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="257b07"

Query Match 0.2%; Score 16.4; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAGAGAGAAAAAGAGAGAAAACAAA 4038

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1211

LOCUS AZ812708/c 27 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M079M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M007M06 R, genomic survey sequence.

ACCESSION AZ358038

VERSION AZ812708

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0079 row: M column: 06
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M007M06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.4; DB 1; Length 27;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAACAAATGTTAT 4045
|||||
Db 26 AAAAAAAAAAAAAAAAAATTTT 1

RESULT 1212
AZ358038 28 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION IM0100F05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0100F05 F, genomic survey sequence.

ACCESSION AZ358038

VERSION AZ358038.1 GI:10471738

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: F column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0100F05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.4; DB 1; Length 28;
Best Local Similarity 76.9%; Pred. No. 1.4e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4018 AAAAAAGAGAAACAAATGTT 4043
|||||
Db 3 AAAAAAAAAAAAAAAAAATTT 28

RESULT 1213
R16114/c 32 bp mRNA linear EST 13-APR-1995
LOCUS
DEFINITION Y551F03.s2 Soares fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:66461 3' similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE

ZETA PRECURSOR (HUMAN); mRNA sequence.
 R16114
 R16114.1 GI:767923
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 32)
 Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL.
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21m13
 High quality sequence stop: 1.
 Location/Qualifiers
 1..32
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:66461"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGAGAGATTAATTAAGTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.2%; Score 16.4; DB 1; Length 32;
 Best Local Similarity 69.0%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4011 TAAATGAGAAAAGAGAAAACAAA 4039
 DB 30 TAAATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1214
 AZ316019 21 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ316019
 DEFINITION 1M0033C05R Mouse 10kb plasmid UGCG1M library Mus musculus genomic clone UGCG1M0033C05 R, genomic survey sequence.
 ACCESSION AZ316019
 VERSION AZ316019.1 GI:10363426
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0033 row: C column: 05
 Seq primer: CACACGAAACAGCATGAC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0033C05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 9.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTT 4479
 DB 21 TGTGTTTTTTTTTTTTTTT 1

RESULT 1215
 AZ345540 21 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ345540
 DEFINITION 1M0080P05F Mouse 10kb plasmid UGCG1M library Mus musculus genomic clone UGCG1M0080P05 F, genomic survey sequence.
 ACCESSION AZ345540
 VERSION AZ345540.1 GI:10424777
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: P column: 05
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0080P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g114732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4463 CTTTCTTTCTTTCTTTCTTTT 4483
DB 1 CTTTCTTTCTTTCTTTCTTT 21

RESULT 1216
A2346717 21 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION
1M0082002P Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0082002 F, genomic survey sequence.
ACCESSION
A2346717
VERSION
A2346717.1 GI:10425954
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: O column: 02
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g114732114[gb]|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 9.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4463 CTTTCTTTCTTTCTTTCTTTT 4483
DB 1 CTTTCTTTCTTTCTTTCTTT 21

RESULT 1217
A2849030 21 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION
2M0150117F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0150117 F, genomic survey sequence.
ACCESSION
A2849030
VERSION
A2849030.1 GI:13032696
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0150 row: 1 column: 17
 Seq primer: CGTTGTAACGACGCCCACT
 Class: plasmid ends
 High quality sequence stop: 21.
FEATURES
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 9.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3627 GGGGCTGGAGAGAGCTAGA 3647
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 DB 1 GGGGAGGAGAGAGAGAGCA 21

RESULT 1218
LOCUS A2978432 21 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0254G15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0254G15 R, genomic survey sequence.
ACCESSION A2978432
VERSION A2978432.1 GI:13849659
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0254 row: G column: 15
 Seq primer: CACACAGAAACAGCATATAC
 Class: plasmid ends
 High quality sequence stop: 21.
FEATURES
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 /organism="Mus musculus"
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 /clone="UUGC2M0254G15"
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 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PMD42n; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 9.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3615 GGGGATGGGCTGGGCTGGG 3635
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 DB 1 GGGGATGGGCTGGGCTGGG 21

RESULT 1219
LOCUS CF318882 22 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-09-C23.g1 OsHDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD-09-C23, mRNA sequence.
ACCESSION CF318882
VERSION CF318882.1 GI:33690643
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhacoidae; Oryzaceae; Oryza.
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix pic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1. .32
/organism="Glossina morsitans morsitans"
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/sub_species="morsitans"
/db_xref="taxon:37546"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.24; Score 16.2; DB 1; Length 32;
Best Local Similarly 72.4%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4018 AGAAAAAGCAGAAACCAATGTTATT 4046
Db 32 AAAAAAAAAAAAAAAAAAACCTTTT 4

RESULT 1224
AZ759642/c

LOCUS
AZ759642 33 bp DNA linear GSS 16-FEB-2001

DEFINITION
IM0552E03R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION
clone UGCG1M0552E03 R, genomic survey sequence.

VERSION
AZ759642

KEYWORDS
AZ759642.1 GI:12866639

SOURCE
GSS.

ORGANISM
Mus musculus (house mouse)

Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (base 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Isilaw,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinsley,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
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Seq primer: CACACAGGAAACGATATGAC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33
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/clone="UGCG1M0552E03"

FEATURES
source


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/sex="Male"
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/notes="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.2%; Score 16.2; DB 1; Length 33;
Best Local Similarity 72.4%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 4011 TAAATGAGAAAAGAGAAACAA 4039

DB 32 TAGAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1225

BX558128/c 33 bp mRNA linear EST 10-OCT-2003
 LOCUS BX558128 Glossina morsitans morsitans adult infected gut Glossina
 DEFINITION morsitans morsitans cDNA clone Tse36g10_p1c, mRNA sequence.

ACCESSION BX558128
 VERSION BX558128.1 GI:33429275

KEYWORDS

SOURCE

ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE

AUTHORS Lehane, M.J., Akcey, S., Gibson, W., Kertoutou, A., Bettman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198

COMMENT

CONTACT: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 REQUEST FOR CLONES, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UM
 All clones with suffix g1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.

FEATURES

source
 1..33
 location/Qualifiers
 /mol_type="mRNA"
 /organism="Glossina morsitans morsitans"
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 /db_xref="taxon:37546"
 /clone="Tse36g10_p1c"

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/tissue_type="adult infected gut"
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gut"  

/notes="country: Zimbabwe; EST from adult gut infected with  

T.brucei"

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Query Match      0.2%; Score 16.2; DB 1; Length 33;
Best Local Similarity 72.4%; Pred. No. 1.8e+03;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 4019 GAAAAAGAGAAAACAAATGTTATT 4047

DB 33 GAAAAAAAAAAAAAAAAAAAAAACTACT 5

RESULT 1226

B0590166 16 bp mRNA linear EST 06-DEC-2002
 LOCUS B0590166 E012844-024-019-K18-T7 MP12-ADIS-024-storage root Beta vulgaris
 DEFINITION cDNA clone 024-019-K18 3-PRIME, mRNA sequence.

ACCESSION B0590166
 VERSION B0590166.1 GI:26119749

KEYWORDS

SOURCE

REFERENCE

AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,
 Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radelof, U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698

COMMENT

CONTACT: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de
 INSERT LENGTH: 16 Std Error: 0.00
 PLATE: 19 row: K column: 18
 SEQ PRIMER: T7: GTAATGACATCACTATAGGCG.

FEATURES

source

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 /clone_lib="MP12-ADIS-024-storage root"
 /notes="Vector: pCMTSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeher Saat-zucht AG Birkbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SPE-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Query Match      0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1227
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 DEFINITION B0592027 16 bp mRNA linear EST 06-DEC-2002
 E012843-024-019-015-T7 MP1Z-ADIS-024-storage root Beta vulgaris
 ACCESSION CDNA clone 024-019-015 3-PRIME, mRNA sequence.
 VERSION B0592027.1 GI:26119790
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
 Plate: 19 row: 0 column: 15
 Seq primer: T7; GTATATGACGACTACTATAGAGC.
 Location/Qualifiers
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 /clone="024-019-015"
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 /note="Vector: PCWVSPO8T6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfeldener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Best
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT 4484
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 vulgaris CDNA clone 024-028-F08 5-PRIME, mRNA sequence.

ACCESSION B0592600
 VERSION B0592600.1 GI:26122183
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 16 Std Error: 0.00
 Plate: 28 row: F column: 08
 Seq primer: SP6; ATTATGCTGACACTATAGAGA.
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 /issue_type="developing root"
 /lab_host="EMDH10B"
 /clone_1ib="MP1Z-ADIS-024-developing root"
 /note="Vector: PCWVSPO8T6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfeldener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Best
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 16 TTTT TTTT TTTT TTTT 1

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 DEFINITION B0592965 16 bp mRNA linear EST 06-DEC-2002
 S01324-024-028-A01-T7 MP1Z-ADIS-024-developing root Beta vulgaris
 ACCESSION CDNA clone 024-028-A01 3-PRIME, mRNA sequence.
 VERSION B0592965
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 16)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
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 cDNA library from sugar beet, library provided by KWS
 Kleinfeldener Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Best
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RPD/GABI-Primary database: http://gabi.rzpd.de"

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H., and Radelet, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
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FEATURES

source

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SP6-SalI-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1230

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DEFINITION E012692-024-022-H07-SP6 MP1Z-ADIS-024-developing root Beta vulgaris

CDNA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION B0595717
B0595717.1 GI:26125300

VERSION EST.

KEYWORDS Beta vulgaris

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H., and Radelet, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE 22362189
PUBMED 12472698

COMMENT Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
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FEATURES

source

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SP6-SalI-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1231

CE279325

LOCUS CE279325 16 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL-05-J09.G1 Rice etiolated leaf plasmaid cDNA library (14ETL)

Oryza sativa cDNA clone 14ETL-05-J09, mRNA sequence.

ACCESSION CE279325
CE279325.1 GI:33656711

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim, J.S., Um, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

JOURNAL COMMENT Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

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/cultivar="Nackdong"

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1232

CF311057

LOCUS CF311057 16 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.

ACCESSION

CF311057

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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line."

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RESULT 1233

CF314377

LOCUS CF314377 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-001.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--02-001, mRNA sequence.

ACCESSION

CF314377

VERSION CF314377.1 GI:33686138

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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line."

Query Match 0.2%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1234

CF315789

LOCUS CF315789 16 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--04-N10.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.

ACCESSION

CF315789

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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derived from rice Histone Deacetylase overexpression
line."

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 Db 1 TTTT TTTT TTTT TTTT 16

RESULT 1235

LOCUS CF316056 16 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--05-D07.b1 OSHDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.

ACCESSION CF316056
 VERSION CF316056.1 GI:33687817
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

location/Qualifiers
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 line."

Query Match 0.2%; Score 16; DB 1; Length 16;
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT 16

RESULT 1236

LOCUS CF317718 16 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--07-I05.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.

ACCESSION CF317718
 VERSION CF317718.1 GI:33689479
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

location/Qualifiers
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 line."

Query Match 0.2%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4479
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RESULT 1237

LOCUS CF318894 16 bp mRNA linear EST 15-AUG-2003
 DEFINITION HP--09-D06.g1 OSHDA1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.

ACCESSION CF318894
 VERSION CF318894.1 GI:33690655
 KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1238

CF320356

LOCUS CF320356 16 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--11-D14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa clone HD--11-D14, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1239

CF327722

LOCUS CF327722 16 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-F06, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
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/organism="Oryza sativa"
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Qy 4464 TTTT TTTT TTTT TTTT TTTT T 4479
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1 TTTT TTTT TTTT TTTT T 16

RESULT 1240

CF327923

LOCUS CF327923 16 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-J18, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

AUTHORS Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--02-J18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTG 4484
|||||
Db 1 TTTT TTTT TTTT TTTG 16

RESULT 1241
CF328223 16 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION
ACCESSION CF328223
VERSION CF328223.1 GI:33804692
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

REFERENCE Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

AUTHORS Large-scale Sequencing Analysis of Rice ESTs

TITLE Unpublished (2003)

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

COMMENT Location/Qualifiers

FEATURES
source Location/Qualifiers

1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-A10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTG 4484
|||||
Db 1 TTTT TTTT TTTT TTTG 16

RESULT 1242
CF333386/c 16 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.
ACCESSION CF333386
VERSION CF333386.1 GI:33815044
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

REFERENCE Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

AUTHORS Large-scale Sequencing Analysis of Rice ESTs

TITLE Unpublished (2003)

JOURNAL Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

COMMENT Location/Qualifiers

1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-E05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4479
|||||
Db 16 TTTT TTTT TTTT TTTT 1

RESULT 1243
BO590128 17 bp mRNA linear EST 06-DEC-2002
LOCUS BO590128
DEFINITION E012843-024-019-E19-T7 MP12-ADIS-024-estorage root Beta vulgaris
ACCESSION CDNA clone 024-019-E19 3-PRIME, mRNA sequence.
VERSION BO590128.1 GI:26119711

KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfach, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radclouf, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PubMed 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaampz@koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 Row: E Column: 19
Seq primer: 17; GTAATACGACCTCATATAGGCG.
Location/Qualifiers
1..17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="taxon:161934"
/db_xref="EMBL:189986"
/clone="024-019-E19"
/lab_host="E. coli DH10B"
/issue_type="storage root"
/clone_lib="MPZ-ADIS-024-storage root"
/note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. Library provided by KWS
Kleinmanleberer Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; Cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polys-CC-NotI-17; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
|||||
1 TTTT TTTT TTTT TTTT 16

RESULT 1244
CF294668 17 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION CF294668
ACCESSION CF294668
VERSION CF294668.1 GI:33663701
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatrionidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--04-E17"
/issue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
|||||
1 TTTT TTTT TTTT TTTT 16

RESULT 1245
CF295988 17 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--06-C17.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION CF295988
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatrionidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--06-C17"
/issue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E. coli DH10B"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4479
|||||
Db 1 TTTT TTTT TTTT TTTT 16

RESULT 1246

CF297251

LOCUS CF297251 17 bp mRNA linear EST 14-AUG-2003
DEFINITION 300GS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

ACCESSION CF297251
VERSION CF297251.1 GI:33666284

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-P12"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT 4484
|||||
Db 1 TTTT TTTT TTTT TTTT 16

RESULT 1247

CF298341

LOCUS CF298341 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CF298341
VERSION CF298341.1 GI:33670102

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-K24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT 4484
|||||
Db 1 TTTT TTTT TTTT TTTT 16

RESULT 1248

CF302447

LOCUS CF302447 17 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CF302447
VERSION CF302447.1 GI:33674208

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-P11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
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 1 TTTT TTTT TTTT TTTT 16

Db

RESULT 1249

CF313013

DEFINITION ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.

ACCESSION

CF313013
 CF313013.1 GI:333684774

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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 Tel: 82 31 330 6193
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 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

SOURCE

1. 17
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--08-P19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABF-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.2%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
 |||||
 1 TTTT TTTT TTTT TTTT 16

Db

RESULT 1250

CF336950

LOCUS CF336950 17 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--07-D04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.

ACCESSION

CF336950
 CF336950.1 GI:33822280

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 17)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

SOURCE

1. 17
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--07-D04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AcJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
 |||||
 1 TTTT TTTT TTTT TTTT 16

Db

RESULT 1251

CF300236

LOCUS CF300236 19 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--04-124.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--04-124, mRNA sequence.

ACCESSION

CF300236
 CF300236.1 GI:33671997

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

SOURCE

1. 19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--04-124"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"

/lab host="E.coli DH10B"
/clone lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with Oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484
|||||
Db 1 TTTT TTTT TTTT TTTT G 16

RESULT 1252

CF309636 19 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--03-008.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--03-008, mRNA sequence.

ACCESSION CF309636
VERSION CF309636.1 GI:33681397
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..19

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--03-008"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484
|||||
Db 1 TTTT TTTT TTTT TTTT G 16

RESULT 1253

CF311668 19 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-A05, mRNA sequence.

ACCESSION CF311668

VERSION CF311668.1 GI:33683429

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..19

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--07-A05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT T 4479
|||||
Db 16 TTTT TTTT TTTT TTTT T 1

RESULT 1254

CF319596 19 bp mRNA linear EST 15-AUG-2003
LOCUS HD--10-C14.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.

ACCESSION CF319596
VERSION CF319596.1 GI:33691357
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1..19

Query Match 0.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 Db 1 TTTT TTTT TTTT TTTT G 16

RESULT 1255
 CF325356 19 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT1--03-A08.g1 ALCMT-overexpressing transgenic rice lambda phage
 DEFINITION cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-A08, mRNA
 sequence.
 ACCESSION CF325356
 VERSION CF325356.1 GI:33798994
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT Nahm B.H.
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 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers
 1..19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT1--03-A08"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="ALCMT-overexpressing transgenic rice lambda
 phage cDNA library (JMT1)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site. mRNA was
 prepared from Arabidopsis thaliana Carboxyl
 methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 Db 1 TTTT TTTT TTTT TTTT G 16

RESULT 1256
 CF299570 20 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa cDNA clone 7LEAF--03-K09, mRNA sequence.
 ACCESSION CF299570
 VERSION CF299570.1 GI:33671331
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT Nahm B.H.
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 YONGIN, KYEONGGI, KOREA
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 FAX: 82 31 321 6355
 EMAIL: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--03-K09"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT T 4479
 |||||
 Db 1 TTTT TTTT TTTT TTTT T 16

RESULT 1257
 CF330490 20 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--06-D16.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--06-D16, mRNA sequence.
 ACCESSION CF330490
 VERSION CF330490.1 GI:33809214
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-D16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484
1 TTTT TTTT TTTT TTTT G 16

RESULT 1258

CF282313 21 bp mRNA linear EST 14-AUG-2003

LOCUS 14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

DEFINITION Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.

ACCESSION CF282313

VERSION CF282313.1 GI:33659700

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretidae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

location/Qualifiers

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL--09-M08"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_1lb="Rice etiolated leaf plasmid cDNA library

(14ETL)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4469 TTTT TTTT TTTT TTTT TTTT G 4484
21 TTTT TTTT TTTT TTTT G 6

RESULT 1259

AZ341108 21 bp DNA linear GSS 29-SEP-2000

LOCUS 1M0073014F Mouse 10kb plasmid UGCM library Mus musculus genomic

DEFINITION clone UGCM0073014 F, genomic survey sequence.

ACCESSION AZ341108

VERSION AZ341108.1 GI:10417030

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Nederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0073 row: 0 column: 14

Seq primer: CGTGTGTAACGACGCGCAGCT

Class: plasmid ends

High quality sequence stop: 21.

location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM0073014"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1lb="Mouse 10kb plasmid UGCM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gil4732114|bp|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.7e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTT 4478-
 Db 16 CTTTTTTTTTTTTT 1

RESULT 1260

AZ963501

LOCUS

DEFINITION 21 bp DNA linear GSS 27-APR-2001
 2M032M07R Mouse 10kb plasmid UGCGM library Mus musculus genomic

ACCESSION AZ963501
 Clone UGCGM0232M07 R, genomic survey sequence.

VERSION AZ963501.1 GI:13834728

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0232 row: M column: 07
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0232M07"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4469 TTTTTTTTTTTTTT 4484
 Db 1 TTTTTTTTTTTTTT 16

RESULT 1261

AZ317017

LOCUS

DEFINITION 22 bp DNA linear GSS 29-SEP-2000
 1M0035P09F Mouse 10kb plasmid UGCGM library Mus musculus genomic

ACCESSION AZ317017
 Clone UGCGM0035P09 F, genomic survey sequence.

VERSION AZ317017.1 GI:10365400

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0035 row: P column: 09
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES

source

1. 22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0035P09"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTT 4478

Db 7 CTTTTTTTTTTTTT 22

RESULT 1262

AW335179 23 bp mRNA linear EST 31-JAN-2000
 LOCUS S44B4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
 ACCESSION AW335179
 VERSION AW335179.1 GI:6831798
 KEYWORDS EST.
 SOURCE Pneumocystis carinii
 ORGANISM Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
 Pneumocystis carinii

REFERENCE 1 (bases 1 to 23)
 AUTHORS Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
 Edman,J.C., Kovacs,J. and Cuenilton,M.
 TITLE Expressed sequence tags from Pneumocystis carinii
 JOURNAL Unpublished (2000)
 COMMENT Contact: Staben C
 School of Biological Sciences
 University of Kentucky
 101 Morgan Building, University of Kentucky, Lexington, KY
 40506-0225, USA
 Tel: 606 257 2161
 Fax: 606 257 1717
 Email: staben@pop.uky.edu.
 Location/Qualifiers

FEATURES

source
 1..23
 /organism="Pneumocystis carinii"
 /mol_type="mRNA"
 /db_xref="taxon:4754"
 /lab_host="E. coli"
 /clone_lib="AGS-1"
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
 P. carinii organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Triol extracted RNA. Oligo dt priming, standard
 conditions described by vendor. Stragtagene. Further
 details see www.uky.edu/Project/Pneumocystie/"

Query Match 0.2%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTT 4479
 Db 1 TTTTTTTTTTTTTT 16

RESULT 1263

CF334146 23 bp mRNA linear EST 18-AUG-2003
 LOCUS JMT--03-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 DEFINITION JMT--03-F05.g1 Oryza sativa cDNA clone JMT--03-F05, mRNA sequence.
 ACCESSION CF334146
 VERSION CF334146.1 GI:33816628
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 23)

REFERENCE 1 (bases 1 to 23)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

FEATURES
 source
 1..23
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--03-F05"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH105"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasminate Carboxyl
 methyltransferase overexpression line."

Query Match 0.2%; Score 16; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTT 4479
 Db 1 TTTTTTTTTTTTTT 16

RESULT 1264

AZ330773/c 23 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ330773/c
 DEFINITION M0056008F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0056008 F, genomic survey sequence.

ACCESSION AZ330773
 VERSION AZ330773.1 GI:10392809
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D. Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0056 row: O column: 08
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES

source
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0056008"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred.No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4469 TTTTGTGTTTGTG 4484
|||||
23 TTTTGTGTTTGTG 8

RESULT 1265
A0257474/C

LOCUS A0257474 24 bp mRNA linear EST 25-APR-2002
DEFINITION A0257474 3'-directed mouse cDNA library Mus musculus cDNA clone

ACCESSION BED0010682 3', mRNA sequence.

VERSION A0257474

KEYWORDS A0257474.1 GI:20322129

SOURCE EST.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)

AUTHORS Kato, K. and Matsuda, R.

JOURNAL Generation of expressed sequence tags from mouse brain

COMMENT Unpublished (2002)

Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takeyama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkatoda@isf-nara.ac.jp,

URL: <http://love2.isf-nara.ac.jp/BD/index.html>.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="BED0010682"

/release_type="Brain"

/clone_lib="3'-directed mouse cDNA library"

Query Match 0.2%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred.No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3271 TTTGTTAAGAGAAATGAAC 3294

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24 TTTGTTAAGAGAAATGAATC 1

RESULT 1266

LOCUS CF327904 24 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--02-J06.D1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--02-J06, mRNA sequence.

ACCESSION CF327904

VERSION CF327904.1 GI:33804058

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 24)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@gsbto.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..24

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--02-J06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred.No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6467 TTTTTCGTTGTAATGAC 6490
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1 TTTTTCGTTTAAATATGC 24

RESULT 1267

LOCUS AZ308225

DEFINITION AZ308225 24 bp DNA linear GSS 29-SEP-2000

1M0011E06F Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0011B06 F, genomic survey sequence.

ACCESSION AZ308225

VERSION AZ308225.1 GI:10348004

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: B column: 06
Seq primer: CGTGTATAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0011E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTGT 4485
| ||||| ||||| ||||| ||||| |||||
Db 1 AGTTTCTGTTCTTTTCTTTTCTTTT 24

RESULT 1268
A2349008 24 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION IM0085013R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0085013 R, genomic survey sequence.
ACCESSION A2349008
VERSION A2349008.1 GI:10428245
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: O column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES
source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0085013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.2%; Score 16; DB 1; Length 24;
Best Local Similarity 79.2%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTGT 4485
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Db 1 AGTTTCTGTTCTTTTCTTTTCTTTT 24

RESULT 1269
A2805931 24 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0067P02R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0067P02 R, genomic survey sequence.
ACCESSION A2805931
VERSION A2805931.1 GI:12966742
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Genomic survey sequence.

ACCESSION AL492371 GI:11867375
 VERSION AL492371.1
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org

DETAILS of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source Location/Qualifiers
 1..26
 /organism="Trypanosoma brucei"
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 /strain="TREU927"
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 Best Local Similarity 79.24; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 4020 AAAAAAGAGAGAAAACAAATGTT 4043
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 Db 2 AAAAAAAAAAAAAAAAAATTTT 25

RESULT 1273
 AU265518/c 26 bp mRNA linear EST 10-MAY-2002
 LOCUS AU265518 VS Dictyostelium discoideum cDNA clone VSF623 5', mRNA sequence.
 ACCESSION AU265518
 VERSION AU265518.1 GI:20524316
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Meda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.
 TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp.

FEATURES
 source Location/Qualifiers
 1..26
 /organism="Dictyostelium discoideum"

/mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
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 /sex="mat A"
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 /clone_1ib="VS"

Query Match 0.24; Score 16; DB 1; Length 26;
 Best Local Similarity 79.24; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 6977 AAAAAACAAACAGATGAGTGCG 7000
 ||||| ||||| ||||| ||||| |||||
 Db 26 AAAAAAAAAAAAAAAAAAGCGCGG 3

RESULT 1274
 R59382/c 27 bp mRNA linear EST 24-MAY-1995
 LOCUS YH17607.81 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:37726 3', similar to gb:M5131 METHYLMALONYL-COA MUTASE PRECURSOR (HUMAN);, mRNA sequence.
 DEFINITION R59382
 VERSION R59382.1 GI:830077
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: polyT not found
 Seq primer: SP6
 High quality sequence stop: 1.

FEATURES
 source Location/Qualifiers
 1..27
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:410267"
 /db_xref="taxon:9606"
 /clone="IMAGE:37726"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_1ib="Soares infant brain IN1B"
 /note="Organ: whole brain; Vector: Lambda BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']
 AACTGGAAGATTGCGCGCGCAGGAATTTTATTTTATTTT 3';
 double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lambda BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.2%; Score 16; DB 1; Length 27;
 Best Local Similarity 79.2%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4016 TGAGAAAAAGAGACAAACAAA 4039
 |||||
 25 TGAAGAAAAAGAAAAAGAAAAA 2

RESULT 1275
 CF298134/c 32 bp mRNA 1linear EST 15-AUG-2003
 LOCUS
 DEFINITION NACL--08-M01.b1 Rice callus plasmid cDNA library (NACL) Oryza
 ACCESSION CF298134
 VERSION CF298134.1 GI:33669895
 KEYWORDS EST.
 SOURCE
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers

1. 32
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--08-M01"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

FEATURES
 source

1. 32
 /organism="Oryza sativa"
 /mol_type="mRNA"
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 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 16; DB 1; Length 32;
 Best Local Similarity 79.2%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4016 TGAGAAAAAGAGACAAACAAA 4039
 |||||
 30 TGAAGAAAAAGAAAAAGAAAAA 7

RESULT 1276
 CF298134/c 19 bp mRNA 1linear EST 15-AUG-2003
 LOCUS
 DEFINITION 7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 ACCESSION CF298134
 VERSION CF298134.1 GI:33669895
 KEYWORDS EST.
 SOURCE
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers

1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers

1. 19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
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 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTT 4482
 |||||
 19 TTTTTCCTTTTTCCTT 1

RESULT 1277
 CF298472

LOCUS CF298472 19 bp mRNA 1linear EST 15-AUG-2003
 DEFINITION 7LEAF--01-001.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 ACCESSION CF298472
 VERSION CF298472.1 GI:33670233
 KEYWORDS EST.
 SOURCE
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 LOCATION/Qualifiers

1. 19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--01-001"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

FEATURES
 source

1. 19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--01-001"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTCTTTTATAT 4482
 1 TTTTCTCTTTTATAT 19

RESULT 1278

AZ345499 19 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0080F06 F, genomic survey sequence.

ACCESSION AZ345499 GI:10424736

VERSION AZ345499.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
 Plate: 0080 row: F column: 06
 Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends
 High quality sequence stop: 19.

Location/Qualifiers

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 /db_xref="taxon:10090"
 /clone="UUGC1M0080F06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTCTTTTATAT 4482
 1 TTTTCTCTTTTATAT 19

RESULT 1279

AZ509929 19 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0354A07 F, genomic survey sequence.

ACCESSION AZ509929 GI:10691245

VERSION AZ509929.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
 Plate: 0354 row: A column: 07
 Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends
 High quality sequence stop: 19.

Location/Qualifiers

1. 19
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 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4467 TTTTCTCTTTTCTTTTGT 4485
 Db 19 TTTTCTCTTTTCTTTTGT 1

RESULT 1282
 AZ786336 19 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0031H17R Mouse 10kb plasmid UGSC1M library Mus musculus genomic
 DEFINITION clone UGSC2M0031H17 R, genomic survey sequence.
 ACCESSION AZ786336
 VERSION AZ786336.1 GI:12923992
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dduw@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: H column: 17
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /strain="C57BL/6J"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGSC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi14732114|gb|AF129072.1)' a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 8.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTCTTTTCTTTTGT 4482
 Db 1 TTTTCTCTTTTCTTTTGT 19

RESULT 1284
 CF331733 20 bp mRNA linear EST 18-AUG-2003
 LOCUS CF331733/c
 DEFINITION NACL--07-P15.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--07-P15, mRNA sequence.
 ACCESSION CF331733
 VERSION CF331733.1 GI:33811693
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 Song,S.I., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Kim,Y.S., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

Query Match 0.2%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
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 /organism="Pneumocystis carinii"
 /mol_type="mRNA"
 /db_xref="taxon:4754"
 /lab_host="E. coli"
 /clone_lib="AGS-1"
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
 P. carinii organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dT priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/pneumocystis/"

REFERENCE
 AUTHORS Edman,J.C., Kovacs,J. and Cushion,M.
 TITLE Expressed sequence tags from Pneumocystis carinii
 JOURNAL Unpublished (2000)
 COMMENT Contact: Staben C
 School of Biological Sciences
 University of Kentucky
 101 Morgan Building, University of Kentucky, Lexington, KY
 40506-0225, USA
 Tel: 606 257 2161
 Fax: 606 257 1717
 Email: staben@pop.uky.edu.
 Location/Qualifiers
 1..20
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 /db_xref="taxon:4754"
 /lab_host="E. coli"
 /clone_lib="AGS-1"
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
 P. carinii organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dT priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/pneumocystis/"

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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1. .20
/organism="Oryza sativa"
/mol_type="mRNA"
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/lab_host="E.coli DH10B"
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Query Match

Best Local Similarity 0.2%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

4460 GCACCTTTTCTTTTCTTTT 4478

Db

19 GCGCTTTTCTTTTCTTTT 1

RESULT 1285

AZ345710/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0080H05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
```

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.2%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

4025 AGAGAGAAAACAAATGTT 4043

Db

20 AGAGAGAAAACCTATGTT 2

RESULT 1286

AZ313243

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUC1M0029H16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
```

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3623 GGGTGGGGTGGGAGAGA 3641
Db 2 GGGTGGGGTGGGAGAGA 20

RESULT 1287

AZ818565/c 21 bp DNA linear GSS 20-FEB-2001
LOCUS 2M088K10R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUCG2M088K10 R, genomic survey sequence.

ACCESSION AZ818565
VERSION AZ818565.1 GI:12988473

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0088 row: K column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M088K10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD2nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4460 GGAATTTTTTTTTTTT 4478
Db 19 GGGGTTTTTTTTTTTT 1

RESULT 1288

CF318882/c 22 bp mRNA linear EST 15-AUG-2003
LOCUS CF318882
DEFINITION HD-09-C23.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD-09-C23, mRNA sequence.

ACCESSION CF318882
VERSION CF318882.1 GI:33690643

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Naim B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahe@bio.com, bhnahe@bio.myongji.ac.kr.

FEATURES

source
1..22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
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/note="Vector: PCR4-TOP0, Site 1: EcoRI, Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5405 GCATTCAGAAATAAAAA 5423
 Db 22 GCATTCAGAAATAAAAA 4

RESULT 1289
 A2711221 23 bp DNA linear GSS 16-FEB-2001
 LOCUS A2711221/c
 DEFINITION 1M0573A16F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0573A16 F, genomic survey sequence.
 ACCESSION A2711221
 VERSION A2711221.1 GI:12893248
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Niedermaier, A., Rose, R., Stokes, R., Tingey, A., von
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niedermaier, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL University of Utah Genome Center
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0573 row: A column: 16
 Seq primer: CGTGTGAAACGACGCCAGCT
 Class: plasmid ends

FEATURES
 source
 location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0573A16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 23;
 Best Local Similarity 89.5%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4460 GGAATTTTATTTTATTTT 4478

Db 19 GCGGTTTTTTTTTTTTT 1

RESULT 1290
 A2314206 24 bp DNA linear GSS 29-SEP-2000
 LOCUS A2314206
 DEFINITION 1M0030H19R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0030H19 R, genomic survey sequence.
 ACCESSION A2314206
 VERSION A2314206.1 GI:10359866
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Niedermaier, A., Rose, R., Stokes, R., Tingey, A., von
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niedermaier, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)
 JOURNAL University of Utah Genome Center
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0030 row: H column: 19
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends

FEATURES
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 location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0030H19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 24;
 Best Local Similarity 89.5%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6004 GAGGTTTCGCGATTTT 6022

Db 5 GGATGTTTCGACCTT 23

RESULT 1291
AZ658569/c 24 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0080M05R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0080M05 R, genomic survey sequence.
ACCESSION AZ658569
VERSION AZ658569.1 GI:10424975
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: M column: 05
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0080M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 4405 TTATCAAAATGATTTT 4423
Db 23 TTTAAAAAATGATTTAT 5

RESULT 1292
AZ658569/c 24 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0535L19F Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM00535L19 F, genomic survey sequence.
ACCESSION AZ658569
VERSION AZ658569.1 GI:11795715
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0535 row: L column: 19
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

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/mol_type="genomic DNA"
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/clone="UGCM00535L19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 24;
Best Local Similarity 89.5%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Gy 5086 TAACATCCATCGCCCTG 5104
Db 23 TCACACCCATCGCCCTG 5

RESULT 1293
 AM327923 27 bp mRNA linear EST 28-JAN-2000
 LOCUS dr02908.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA
 DEFINITION sequence.
 ACCESSION AM327923
 VERSION AM327923.1 GI:6798418
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 27)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Edge Biosystems
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Place: LNCM0029 row: M column: 16
 Seq primer: -21m3 forward primer (ABI).
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847159"
 /tissue_type="Burkitt lymphoma"
 /cell_line="MGC4"
 /clone_1ib="NIH_MGC_3"
 /note="Organ: lymph; Vector: pOTB7a; Library prepared by
 Edge Biosystems."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAGAAACAA 4038
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1294
 CF291968 27 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 DEFINITION sativa cDNA clone 14ROOT--02-J21, mRNA sequence.
 ACCESSION CF291968
 VERSION CF291968.1 GI:33661001
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacridae; Oryzaceae; Oryza.
 1 (bases 1 to 27)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

FEATURES
 source
 1..27
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--02-J21"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AAATGAGAAAAAGAGAGAAACAA 4039
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1295
 CF299084 27 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa cDNA clone 7LEAF--02-P02, mRNA sequence.
 ACCESSION CF299084
 VERSION CF299084.1 GI:33670845
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacridae; Oryzaceae; Oryza.
 1 (bases 1 to 27)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of BioScience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..27
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--02-P02"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AAATGAGAAAAAGAGAGAAACAA 4039
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1296
CF329725/c 27 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--05-C12, mRNA sequence.
ACCESSION CF329725
VERSION CF329725.1 GI:33807665
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.
1 (bases 1 to 27)
Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/culivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAAA 4038
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1297
CF330557/c 27 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--06-F04, mRNA sequence.
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.
1 (bases 1 to 27)
Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Query Match 0.2%; Score 15.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAAA 4038
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1298
CF335229/c 27 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--04-N08.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--04-N08, mRNA sequence.
ACCESSION CF335229
VERSION CF335229.1 GI:33818810
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretidae; Oryzaceae; Oryza.
1 (bases 1 to 27)
Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/culivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--04-N08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAAA 4038

RESULT 1301
 AZ486791/c
 LOCUS 27 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0315K21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0315K21 F, genomic survey sequence.
 ACCESSION
 AZ486791
 VERSION
 AZ486791.1 GI:10653911
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: K column: 21
 Seq primer: CGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 27.
 FEATURES
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 1..27
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0315K21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGAAACAA 4038
 Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1302
 AZ511894/c
 LOCUS 27 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0357E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0357E11 F, genomic survey sequence.
 ACCESSION
 AZ511894
 VERSION
 AZ511894.1 GI:10693210
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0357 row: E column: 11
 Seq primer: CGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 27.
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 1..27
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0357E11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 4012 AAAATGAGAAAAAGAGAAACAA 4038
 Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1303
 AZ580921/c
 LOCUS 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0395924F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0369524 F, genomic survey sequence.
 ACCESSION AZ580921
 VERSION AZ580921.1 GI:11695417
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 REFERENCE 1 Dum,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0369 row: E column: 24
 Seq primer: CCGTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0369524"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAGAGAGAAACAA 4038
 |||||
 DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1304

AZ616094/c
 LOCUS 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0445E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0445E17 R, genomic survey sequence.
 ACCESSION AZ616094
 VERSION AZ616094.1 GI:11738284
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 REFERENCE 1 Dum,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0445 row: E column: 17
 Seq primer: CACACGAAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0445E17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAGAGAGAAACAA 4038
 |||||
 DB 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1305
 AZ623186/c

LOCUS A2623186 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0460D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0460D12 R, genomic survey sequence.
 ACCESSION A2623186
 VERSION A2623186
 KEYWORDS A2623186.1 GI:11745376
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weis,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0460 row: D column: 12
 Seq primer: CACACGAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0460D12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Oy 4012 AAAATGAGAAAAAGAGAAAAACAA 4038
 ||||| ||||| ||||| ||||| |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 1306
 A2627847/c 27 bp DNA linear GSS 13-DEC-2000
 LOCUS A2627847

DEFINITION IM0474011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0474011 F, genomic survey sequence.
 ACCESSION A2627847
 VERSION A2627847
 KEYWORDS A2627847.1 GI:11750133
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weis,R.
 Title Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0474 row: O column: 11
 Seq primer: CGTTGTAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0474011"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 Oy 4012 AAAATGAGAAAAAGAGAAAAACAA 4038
 ||||| ||||| ||||| ||||| |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 1307
 A2809295 27 bp DNA linear GSS 20-FEB-2001
 LOCUS A2809295
 DEFINITION 2M0073B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0073B15 F, genomic survey sequence.

ACCESSION AZ809295
 VERSION AZ809295.1 GI:12975450
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0073 row: B column: 15
 Seq primer: CCTGTAAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0073B15"
 /sex="Male"
 /lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FMD2nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 74.1%; Score 15.8; DB 1; Length 27;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038
 |||||
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

Db
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1308
 TA355B06P 27 bp DNA linear GSS 13-DEC-2000
 LOCUS TA355B06P
 DEFINITION T. brucei sheared genomic DNA clone 355b06, forward sequence,
 genomic survey sequence.

AL493923
 VERSION AL493923.1 GI:11870552
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 27)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="355B06"

Query Match
 Best Local Similarity 74.1%; Score 15.8; DB 1; Length 27;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038
 |||||
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

Db
 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1309
 AZ941721 27 bp DNA linear GSS 26-APR-2001
 AZ941721/c
 LOCUS AZ941721/c
 DEFINITION 2M0201004R Mouse 10kb plasmid UUGC2M library mus musculus genomic
 clone UUGC2M0201004 R, genomic survey sequence.
 ACCESSION AZ941721
 VERSION AZ941721.1 GI:13804440
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
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 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: 0 column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

Location/Qualifiers

1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2M0201004"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG2M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAGAGAACAA 4038
Db 27 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1310

AZ434285

LOCUS 27 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0220B08R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0220B08 R, genomic survey sequence.

ACCESSION

AZ434285

VERSION

AZ434285.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weis,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0220 row: B column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0220B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAGAGAACAA 4038
Db 1 AAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1311

AZ458228

LOCUS 27 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0262C12F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0262C12 F, genomic survey sequence.

ACCESSION

AZ458228

VERSION

AZ458228.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weis,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0262 row: C column: 12

Seq primer: CGTGTGTAAGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC1M0262C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 27;
 Best Local Similarity 74.1%; Pred. No. 1.6e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1312
 LOCUS AL048439 28 bp mRNA linear EST 04-SEP-2003
 DEFINITION DKFZps8611924_r1 586 (synonym: hute1) Homo sapiens cDNA clone
 ACCESSION AL048439
 VERSION AL048439
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 28)
 Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
 EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany.
 Location/Qualifiers
 1.28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZps8611924"
 /release_type="uteras"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="586 (synonym: hute1)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

Query Match 0.2%; Score 15.8; DB 1; Length 28;
 Best Local Similarity 74.1%; Pred. No. 1.7e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 1313
 LOCUS CF322082 28 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD-13-123_g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD-13-123, mRNA sequence.
 ACCESSION CF322082
 VERSION CF322082
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 28)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomic and Genetic Institute, Greengene Biotech Inc.; Division of BioScience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1.28
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-13-123"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E. coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

FEATURES
 source

Query Match 0.2%; Score 15.8; DB 1; Length 28;
 Best Local Similarity 74.1%; Pred. No. 1.7e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1314
 LOCUS CF337400 28 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--07-N04_g1 AJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-N04, mRNA sequence.
 ACCESSION CF337400
 VERSION CF337400.1 GI:33823200
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

FEATURES
source
location/Qualifiers
1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT-07-N04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AluMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-NOPO. Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonic Acid Carboxyl
methyltransferase overexpression line."

Query Match 0.24; Score 15.8; DB 1; Length 28;
Best Local Similarity 74.1%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4011 TAAATGAGAAAAAGAGAAACAA 4037
Db 2 TAAAAAAAAAAAAAAAAAAAAA 28

RESULT 1315
AZ481286/c 28 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0303L24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0303L24 F, genomic survey sequence.
ACCESSION AZ481286.1 GI:10642351
VERSION
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0303 row: L column: 24
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source
location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0303L24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1472114|gp|A129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.24; Score 15.8; DB 1; Length 28;
Best Local Similarity 74.1%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4010 CTAAATGAGAAAAAGAGAAACCA 4036
Db 28 CAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1316
T56352/c 28 bp mRNA linear EST 06-FEB-1995
LOCUS y34c09.g1 Striatagene fetal spleen (#937205) Homo sapiens cDNA
DEFINITION clone IMAGE:73072.3' similar to gb:S41458 ROD
CGMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN),
mRNA sequence.
ACCESSION T56352
VERSION T56352.1 GI:658213
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 28)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, W.,
Hawkins, M., Huilman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohtling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaekis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
TITLE
JOURNAL MEDLINE
PUBMED
COMMENT
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1

Source: IMAGE Consortium, LNLN.
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21m13
High quality sequence stop: 1.

FEATURES

source
1. 28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:494737"
/db_xref="taxon:9606"
/clone="IMAGE:73072"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene fetal spleen (#937205)"
/note="Organ: Spleen; Vector: pBluescript SK-; Site: 1;
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled spleens. Average insert size: 1.0 kb;
unt-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACG
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

Query Match
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4012 AAAAAAGAAAAAGAGAAAAACAAA 4039
DB 28 AAAAAAAAAAAAAAAAAATNAAA 1

RESULT 1317

LOCUS AZ825156 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0100N08F Mouse 10kb plasmid UGCM1 library Mus musculus genomic
clone UGCM20100N08 F, genomic survey sequence.
ACCESSION AZ825156
VERSION AZ825156.1 GI:12995064
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islem, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: N column: 08
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES

source
1. 29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM20100N08"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM1 library"
/note="Vector: PMD42n; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI:47321419b/AF12907.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 74.1%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AATATGAAAAAGAGAAAAACAAA 4039
DB 1 AAAAAAAAAAAAAAAAAATNAAA 27

RESULT 1318

LOCUS B0583967/c 29 bp mRNA linear EST 06-DEC-2002
DEFINITION B013297-024-004-B01-77 MP12-ADIS-024-inflorescence Beta vulgaris
CDNA clone 024-004-B01 3-PRIME, mRNA sequence.
ACCESSION B0583967
VERSION B0583967.1 GI:26113544
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 29)
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL Contact: Weishaar B
COMMENT ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mplz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Seq primer: T7; GTAATACGACTCATTATGAGC.
High quality sequence stop: 29.

FEATURES

source
1. 29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:182728"
/db_xref="taxon:161934"
/clone="024-004-B01"
/tissue_type="inflorescence"
/lab_host="EMDH10B"

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2
Query Match	Best Local Similarity	74.1%	Pred. No. 1.7e+03	30 bp	linear
Matches	20; Conservative	0; Mismatches	7; Indels	0; Gaps	0;
Db	4012	AAAAATGAGAAAAAGAGAAAAACAAA	4038		
RESULT 1319	BX554779/C				
LOCUS	BX554779				
DEFINITION	BX554779				
ACCESSION	BX554779				
KEYWORDS	BX554779.1				
SOURCE	EST.				
ORGANISM	Glossina morsitans morsitans				
REFERENCE	Lehane, M.J., Aksey, S., Gibson, W., Kershorn, A., Bettiman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.				
AUTHORS	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes				
TITLE	Genome Biol. 4 (10), R63 (2003)				
JOURNAL	22881942				
MEDLINE	14519198				
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..30 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tset17d12_p1c" /tissue_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"				
FEATURES	source				
Query Match	Best Local Similarity	74.1%	Pred. No. 1.8e+03	30 bp	linear
Matches	20; Conservative	0; Mismatches	7; Indels	0; Gaps	0;
Db	4012	AAAAATGAGAAAAAGAGAAAAACAAA	4038		
RESULT 1319	BX554779/C				
LOCUS	BX554779				
DEFINITION	BX554779				
ACCESSION	BX554779				
KEYWORDS	BX554779.1				
SOURCE	EST.				
ORGANISM	Glossina morsitans morsitans				
REFERENCE	Lehane, M.J., Aksey, S., Gibson, W., Kershorn, A., Bettiman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.				
AUTHORS	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes				
TITLE	Genome Biol. 4 (10), R63 (2003)				
JOURNAL	22881942				
MEDLINE	14519198				
COMMENT	Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end. Location/Qualifiers 1..30 /organism="Glossina morsitans morsitans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clone="Tset17d12_p1c" /tissue_type="adult infected gut" /clone_lib="Glossina morsitans morsitans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"				
FEATURES	source				

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Db      | 30 AAAAAAAAAAAAAAAAAA CTTTA 4
RESULT 1320
A2326012
LOCUS   A2326012          32 bp     DNA             linear    GSS 29-SEP-2000
DEFINITION Mus musculus uTGCIM library Mus musculus genomic clone UGCGIM0048A19 R, genomic survey sequence.
ACCESSION A2326012
VERSION   A2326012.1
KEYWORDS  GI:10363271
SOURCE    GSS.
ORGANISM  Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R., Tingley,A., von Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts
TITLE     Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT   University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
          Tel.: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0048 row: A column: 19
          Seq primer: CACACAGCAACAACGTATGACC
          Class: plasmid ends
          High quality sequence stop: 32.
FEATURES
         Location/Qualifiers
            1..32
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UGCGIM0048A19"
                /sex="male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /cclone_1lb="Mouse 10kb plasmid uTGCIM library"
                /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA was hydromedically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [GI4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match      0.28; Score 15.8; DB 1; Length 32;
Best Local Similarity 74.1%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

Db 5 AACCAAAAAAAAAAAAAAAAAAAAA 31

RESULT 1321
TA264B08P 38 bp DNA linear GSS 13-DEC-2000
LOCUS TA264B08P/c
DEFINITION T. brucei sheared genomic DNA clone 264b08, forward sequence,
genomic survey sequence.
ACCESSION AL483993
VERSION AL483993.1 GI:11849953
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 38)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..38
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="264b08"

Query Match 0.2%; Score 15.8; DB 1; Length 38;
Best Local Similarity 74.1%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAAACA 4038
Db 38 AAAAAAAAAAAAAAAAAAAAAA 12

RESULT 1322
AZ770047 42 bp DNA linear GSS 16-FEB-2001
LOCUS AZ770047
DEFINITION 1M0571B19F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0571B19 F, genomic survey sequence.
ACCESSION AZ770047
VERSION AZ770047.1 GI:12890825
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weisb., R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: B column: 19
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0571B19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_1b="mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.8; DB 1; Length 42;
Best Local Similarity 65.7%; Pred. No. 1.8e+03;
Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2459 GCAGCGACGACGATCCAGGCGACCGACCA 2493
Db 42 GCAGCGACGACGACGCGACGCGACGACGCA 8

RESULT 1323
TA303G05P 22 bp DNA linear GSS 13-DEC-2000
LOCUS TA303G05P
DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence,
genomic survey sequence.
ACCESSION AL497383
VERSION AL497383.1 GI:11865504
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TRU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The *v* + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
source

Source

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1. .22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="303g05"
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Query Match	0.2%	Score 15.6;	DB 1;	Length 22;
Best Local Similarity	81.8%;	Pred. NO. 1.2e+03;		
Matches 18;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

QY 4018 AGAAAAAAAAAGACAGAAAAACA AAAA 4039
| | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAGAAAAAAAAAAA 22

RESULT 1324

LOCUS AA599803 22 bp mRNA linear EST 05-JUN-1998
DEFINITION osa10d4.b1 NC1 CGAP Br2 Homo sapiens cDNA clone IMAGE:1607911 3'
similar to TR:Q34192 Q34192 NADH DEHYDROGENASE SUBUNIT 5.; mRNA
sequence.

ACCESSION	AA999803	
VERSION	AA999803.1	GI:3190358
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 22)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

**JOURNAL
COMMENT**

Tumor Gene Index
Unpublished (1997)
Contact: Robert Straube, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R
Emmert-Buck, M.D., Ph.D.
CNA Library Preparation: M. Bento Soares, Ph.D.

Trace considered overall poor quality
Seq primer: -40mJ3 fwd: ET from Amersham
High quality sequence: stop: 1.
www-bio.1nl.gov/bbrp/image/image.html

FEATURES

source

```

1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:3606"
/clone="TMAGB:1607911"
/sex="female, pooled"
/tissue_type="Dbreast"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Br2"
/note="Vector: pT7AD-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk

```

breast tumor tissue, and was then primed with a Not I - oligo(dT)₁₈ primer. Double-stranded cDNA was ligated to EcoRI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. This library is the normalized version of NotI CGAP-Brl. Library was constructed by Bento Soares and M. Fatima Bonalido. "

Query Match	0.2%;	Score 15.6;	DB 1;	length 22;
Best Local Similarity	81.8%;	Pred. No. 1.2e+03;		
Matches 18;	Conservative	0;	Mismatches 4;	Indels 0;
				Gaps 0;

QY	4464	TTTTTTTTTTTTTTTTTTGT	4485
Db	1	TTTGTGTTTGTGCTTTGT	22

RESULT 1325
CF300339

LOCUS	CE300339	22 bp	mRNA	linear	EST 15-AUG-2003
DEFINITION	7LEAF--04-L05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza				
	sativa cDNA clone 7LEAF--04-L05, mRNA sequence.				

ACCESSION	CF300339	GI:33672100
VERSION	CF300339.1	
KEYWORDS	EST.	
SOURCE	Oryza sativa	
ORGANISM	Oryza sativa	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (Pages 1 to 2)
AUTHORS Kim, J. S., Jun, K. M., Cheong, P. U., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 22

FEATURES
source

FEATURES
SOURCE

Source

```

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-L05"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E. coli DH10B"
/clone_1lb="Rice leaf cDNA library II (7LEAF)"
/note="Vector: PCR-10FO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.2%	Score 15.6	DB 1	Length 22
Best Local Similarity	81.8%	Pred. No. 1.2e+03		
Matches 18	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY	4466	TTTTTTTTTTTTTTTTTTGCT	4487
Db	1	TTTTTTTTTTTTTCTAGTT	22

RESULT 1326
AZ471736/C

LOCUS	22 bp	DNA	1 linear	GSS 04-OCT-2000
DEFINITION	AZ471736			
	1M0286112R	Mouse 10kb plasmid	UUCG1M library	Mus musculus genomic
	clone UUCG1M0286112 R,	genomic survey	sequence.	

ACCESSION	AZ471736
VERSION	AZ471736.1
	GI:10629957

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0286 row: 1 column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1. 22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCTM0286112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4462 ACCTTTTATGCTTTT 4483
Db 22 ATTTTATGCTTTT 1

RESULT 1327
AZ592068/c 22 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION 1M0402H08 Mouse 10kb plasmid UGCIM library Mus musculus genomic
ACCESSION AZ592068
VERSION AZ592068.1 GI:11714258
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: H column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1. 22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCTM0402H08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7443 GGTGTTTAAAGACACAGT 7464
Db 22 GTGTTGCAATACACAGTG 1

RESULT 1328
AZ633751 22 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION 1M048911F Mouse 10kb plasmid UGCIM library Mus musculus genomic
ACCESSION AZ633751
VERSION AZ633751.1 GI:11755941
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0489 row: 1 column: 11
Seq primer: CTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0489111"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gbl]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5327 TCTCTTTTGGCTCCTCTCTC 5348
Db 1 TCTCTCTCTCTCTCTCTCTC 22

RESULT 1329
LOCUS TAI89G04P/c 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 189g04, forward sequence,
genomic survey sequence.
ACCESSION AL477750.1 GI:11841701
VERSION GSS.
KEYWORDS Trypanosoma brucei
SOURCE Trypanosoma brucei

REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Ackin,R., Chillingworth,C., Ormond,D., Harrie,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submissions
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="189904"

Query Match 0.2%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5318 CTCTCTTTTCTCTCTTTGCTT 5339
Db 22 CTCTCTTTGCTCTTTTGCT 1

RESULT 1330
LOCUS A2486853/c 23 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0315M1R Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0315M14 R, genomic survey sequence.
ACCESSION A2486853
VERSION A2486853.1 GI:10654033
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weis,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 14
Seq primer: CACACAGAAACGACTATGACC
Class: plasmid ends
High quality sequence stop: 23.

sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nrls.go.jp>)"

Query Match 0.2%; Score 15.6; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4027 AGAGAAACAAATGTATTTT 4049
Db 23 AGAGATTAAGTTTATTTT 1

RESULT 1333

AZ618720/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0450 row: O column: 19

Seq primer: GGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0450019"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3622 GCGGTGCGGTGCGAGAGAGC 3643
Db 23 GCGGGGGGGGGGGGGGAGC 2

RESULT 1334

AZ793326/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0046 row: B column: 04

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

FEATURES

source

1..23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0046B04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUC2M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 3622 GCGGTGCGGTGCGAGAGAGC 3643
Db 23 GCGGGGGGGGGGGGGGAGC 2

and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGAGAGAGG 3643
|||||
Db 22 GGGGTGGGGTGGGGGGGGG 1

RESULT 1335
AZ822888 23 bp DNA linear GSS 20-FEB-2001
LOCUS AZ822888/c

DEFINITION 2M0265123F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0265123 F, genomic survey sequence.

ACCESSION AZ822888
VERSION AZ822888.1 GI:12992796
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL Contract: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0096 row: G column: 06
Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 23.

Location/Qualifiers
1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096G06"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was ligated to the blunt ends in high molar excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

Query Match 0.2%; Score 15.6; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5327 TCTCTTGGCTCACTCTC 5348
|||||
Db 22 TCTCTCTCTCTCTCTCTC 1

RESULT 1336
AZ984045 23 bp DNA linear GSS 27-APR-2001
LOCUS AZ984045

DEFINITION 2M0265123F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0265123 F, genomic survey sequence.

ACCESSION AZ984045
VERSION AZ984045.1 GI:13855272
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE 1 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL Contract: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0265 row: I column: 23
Seq primer: CGTGTAAACAGCAGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

Location/Qualifiers
1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0265123"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was ligated to the blunt ends in high molar excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

JOURNAL
COMMENT

Unpublished (1999)
Other ESTs: 2821537.Sprime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNLN) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNLN at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 14
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LICM7 row: B column: 2
High quality sequence stop: 14.
Location/Qualifiers

FEATURES

source

```
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821537"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_7"
/notes="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match

Best Local Similarity 0.2%; Score 15.6; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4476 TTTTTCCTTGTGACATCG 4497

Db 1 TTTTTCCTTGTGACATCG 22

RESULT 1340
AW248929/c

LOCUS 24 bp mRNA linear EST 07-JAN-2000
DEFINITION 2819212.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819212 3',
mRNA sequence.

ACCESSION AW248929

VERSION AW248929.1 GI:6591922

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 24)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2819212.Sprime
Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNLN) DNA Sequencing by: Berkeley MGC sequencing

FEATURES

source

project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNLN at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LICM1 row: A column: 5
High quality sequence stop: 10.
Location/Qualifiers

Query Match

Best Local Similarity 0.2%; Score 15.6; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4018 AGAAAAAGAGAGAAACAAA 4039

Db 24 AGAAAAAGAGAGTAAAAAAA 3

RESULT 1341
AZ404465

LOCUS 24 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0172P09R Mouse 10kb plasmid UNGCM library Mus musculus genomic
clone UNGCM0172P09 R, genomic survey sequence.

ACCESSION AZ404465

VERSION AZ404465.1 GI:10528394

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0172 row: P column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

source

1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0172P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 24;
Best Local Similarity 81.8%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Gy 3622 GGGGTGGGGTGGAGAGAGG 3643
Db 2 GGGGGGGGGGAGAGAGGGG 23

RESULT 1342
AZ404078 25 bp DNA linear GSS 03-OCT-2000
LOCUS 1M017207F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M017207 F, genomic survey sequence.
ACCESSION AZ404078
VERSION AZ404078.1 GI:10528091
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: J column: 07

Seq primer: CGTTGTAAAGACGGCCACT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES

source

1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0172J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.6; DB 1; Length 25;
Best Local Similarity 81.8%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Gy 4018 AGAAAAAGAGAGAAACAAA 4039
Db 4 AAAAAAAAAAGAAAAAAAAA 25

RESULT 1343
AM249476/c 25 bp mRNA linear EST 07-JAN-2000
LOCUS 2821131.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821131 3',
DEFINITION mRNA sequence.
ACCESSION AM249476
VERSION AM249476.1 GI:6592469
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 25)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821131.Sprime
Contact: Robert Strauberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNU) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNU at:
www-bio.lind.gov/bdrp/image/image.html Base Calling / Quality
Scores: PHRD from University of Washington Genome Center
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-P Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu> Low Quality Sequence: 25
contiguous PHRD high quality bases following vector sequence. Very

Query Match 0.2%; Score 15.6; DB 1; Length 27;
 Best Local Similarity 81.8%; Pred. No. 1.7e+03;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAACAAA 4039
 |||||
 Db 26 AGAAAAAGAGAAACAAA 5

RESULT 1346
 AL587570/c 32 bp mRNA linear EST 02-MAR-2001
 LOCUS AL587570 BP Chicken Brain Library Gallus gallus cDNA clone
 DEFINITION ROS059B09, mRNA sequence.
 ACCESSION AL587570
 VERSION AL587570.1 GI:13192604
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Murray, F.
 TITLE BP Chicken Brain Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Fraser Murray
 Dept. Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UK
 Tel: +44 (0)131 527 4200
 Fax: +44 (0)131 440 0434
 Email: frazer.murray@bbsrc.ac.uk
 GCGGCGCTTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
 (*6854-
 Seq primer: M13P.
 FEATURES
 source Location/Qualifiers
 1..32
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="ROS059B09"
 /tissue_type="Brain"
 /dev_stage="Unknown"
 /lab_host="DH10B"
 /clone_lib="BP Chicken Brain Library"
 /note="Vector: pSPORT1, Site 1: NotI, Site 2: SalI, Cloned
 unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
 5' TGACCTCGAG 3' ; 3' adaptor sequence: 5'
 GCGGCGCTTTT TTTT TTTT 3' Poly A RNA purchased from
 Clontech (*6854-1)"

Query Match 0.2%; Score 15.6; DB 1; Length 32;
 Best Local Similarity 81.8%; Pred. No. 1.9e+03;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAACAAA 4039
 |||||
 Db 25 AGAAAAAGAGAAACAAA 4

RESULT 1347
 BX556508/c 35 bp mRNA linear EST 10-OCT-2003
 LOCUS BX556508 Glosina morsitans morsitans adult infected gut Glosina
 morsitans morsitans cDNA clone Tse27f04_plc, mRNA sequence.
 ACCESSION BX556508
 VERSION BX556508.1 GI:33427768
 KEYWORDS EST.
 SOURCE Glosina morsitans morsitans
 ORGANISM Glosina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

REFERENCE 1 (bases 1 to 35)
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glosina
 morsitans morsitans and expression analysis of putative immune
 response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix plc are reverse primer reads starting at 5'
 end of the cDNA all plc reads are from
 the 3' end.
 FEATURES
 source Location/Qualifiers
 1..35
 /organism="Glosina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse27f04_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glosina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T. Brucei"

Query Match 0.2%; Score 15.6; DB 1; Length 35;
 Best Local Similarity 81.8%; Pred. No. 2e+03;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAAACAAA 4039
 |||||
 Db 32 AGAAAAAGAGAAACAAA 11

RESULT 1348
 BX531095/c 37 bp mRNA linear EST 10-OCT-2003
 LOCUS BX531095 Glosina morsitans morsitans adult infected gut Glosina
 morsitans morsitans cDNA clone Tse127c07_plc, mRNA sequence.
 ACCESSION BX531095
 VERSION BX531095.1 GI:33377293
 KEYWORDS EST.
 SOURCE Glosina morsitans morsitans
 ORGANISM Glosina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossiniidae; Glosina.
 REFERENCE 1 (bases 1 to 37)
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glosina
 morsitans morsitans and expression analysis of putative immune
 response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane

Query Match 0.2%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1351

BQ591588

LOCUS 17 bp mRNA linear EST 06-DEC-2002
 DEFINITION B012616-024-017-C15-SP6 MP12-ADIS-024-storage root Beta vulgaris

ACCESSION BQ591588
 VERSION BQ591588.1 GI:26121171

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris
 Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

REFERENCE
 AUTHORS
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698

COMMENT

Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpik-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 17 row: C column: 15
 Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
 Location/Qualifiers

FEATURES

source

1..17
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KMS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:188532"
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 /clone="024-017-C15"
 /issue_type="storage root"
 /lab_host="EMDH10B"
 /clone_id="MP12-ADIS-024-storage root"
 /note="Vector: PCMVSPORt6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KMS
 Kleinwanzlebener Saatgut AG Bieleck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1352
 CF276637/c 17 bp mRNA linear EST 14-AUG-2003
 LOCUS
 DEFINITION 14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--01-N18, mRNA sequence.
 ACCESSION CF276637
 VERSION CF276637.1 GI:33654023
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

FEATURES

source

1..17
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ETL--01-N18"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_id="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 17 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1353

CF291802

LOCUS 17 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
 ACCESSION CF291802
 VERSION CF291802.1 GI:33660835

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-I22"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 8.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1357

CF326845/c

LOCUS NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION bativa cDNA clone NACL--01-B12, mRNA sequence.

ACCESSION CF326845

VERSION CF326845.1 GI:33801944

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--01-B12"
/issue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 19 TTTT TTTT TTTT TTTT TTTT 3

RESULT 1358

AZ447251

LOCUS 19 bp DNA linear GSS 04-OCT-2000

DEFINITION M0244J19F Mouse 10kb plasmid UGCM library Mus musculus genomic

clone UGCM0244J19 F, genomic survey sequence.

ACCESSION AZ447251

VERSION AZ447251.1 GI:10599050

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,

Niederhauser,A. and Wright,D.,Weiss,R., Tingey,A., von

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Place: 0244 row: 3 column: 19

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM0244J19"
/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 9.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4480
 Db 1 TTTT TTTT TTTT TTTT 17

RESULT 1359
 AZ316368/c
 LOCUS
 DEFINITION 20 bp DNA linear GSS 29-SEP-2000
 1M0034122F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0034122 F, genomic survey sequence.

ACCESSION
 AZ316368
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Niederhauser, A., and Wright, D., Weiss, R.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0034 row: L column: 22
 Seq primer: CATTCTTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0034122"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTT TTTT TTTT TTTT 4478

Db 17 AATT TTTT TTTT TTTT 1

RESULT 1360
 AZ369092/c
 LOCUS
 DEFINITION 20 bp DNA linear GSS 02-OCT-2000
 1M0119E01R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0119E01 R, genomic survey sequence.

ACCESSION
 AZ369092
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Niederhauser, A., and Wright, D., Weiss, R.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0119 row: E column: 01
 Seq primer: CACACAGAAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
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 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0119E01"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3338 TTCAGATCCAGTTGT 3354

Db 19 TTAGATCCAGTTGT 3

RESULT 1361

CP330439

LOCUS CP330439 21 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--06-C12.b1 Rice callus cDNA library (NACL) Oryza

ACCESSION CP330439

VERSION CP330439.1 GI:33809110

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..21

/organism="Oryza sativa"

/mol_type="mRNA"

/culivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--06-C12"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI, mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1362

AZ831993

LOCUS AZ831993 21 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0112M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112M01 F, genomic survey sequence.

ACCESSION AZ831993

VERSION AZ831993.1 GI:13001901

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)

AUTHORS Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: M column: 01
Seq primer: CGTTGTAAACGACGCCACT
Clase: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0112M01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 7413 CAGCAGCAGCAGCAGCA 7429

Db 5 CAGCAGCAGCAGCAGCA 21

RESULT 1363

AZ843343

LOCUS AZ843343 21 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142K10 F, genomic survey sequence.

ACCESSION AZ843343

VERSION AZ843343.1 GI:13013251

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.4; DB 1; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4024 AAGAGAGAAACAAATGTTATTT 4048
Db 1 AAAAAAAAAAAAAAAAAATTTTTT 25

RESULT 1366

CF299646 26 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L24.b1 Rice leaf plasmid DNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L24, mRNA sequence.
ACCESSION CF299646
VERSION CF299646.1 GI:33671407
KEYWORDS EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Yonsei University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

COMMENT

Location/Qualifiers

FEATURES

SOURCE

1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/culivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-L24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOP0, Site 1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 26;
Best Local Similarity 76.0%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4015 ATGAGAGAGAGAGAGAGAGAG 4039
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1367
TN236D08P 26 bp DNA linear GSS 13-DEC-2000
LOCUS T1.brucei sheared genomic DNA clone 236d08, forward sequence,
genomic survey sequence.
DEFINITION
ACCESSION AL482943
VERSION AL482943
KEYWORDS
SOURCE
ORGANISM

REFERENCE

1 (bases 1 to 26)
Hall N., Bowman S., Lennard N.J., Doggett J., Ackin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Melville S.B., Rajadream M.A. and Barrell B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
mls@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The V + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: melsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

SOURCE

1..26
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="236d08"

Query Match 0.2%; Score 15.4; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4021 AAGAGAGAGAGAGAGAGAGAG 4046
Db 1 AAAAAAAAAAAAAAAAAATTTTTT 26

RESULT 1368

N29432 27 bp mRNA linear EST 05-JAN-1996
LOCUS N29432/c
DEFINITION y86h10.81 Soares placenta 8x9weeks 2bshb8c9w Homo sapiens CDNA
clone IMAGE:259171.3' similar to gp:564559 TERPANEPTIN PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION N29432
VERSION N29432.1 GI:1147952
KEYWORDS EST.
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 27)
Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaekle E., Waterston R., Williamson A., Wohlmann P. and
Wilson R.
The WashU-Merck EST Project
Unpublished (1995)

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu

FEATURES

source

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.

Location/Qualifiers

1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:388877"
/db_xref="taxon:9606"
/clone="IMAGE:259171"
/dev_stage="Two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo (dt) primer [5'
TGTTACCACTGACAGTGGAGCGCGGATTTTCTTTT 3']"
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."

Query Match

Best Local Similarity 76.0%; Score 15.4; DB 1; Length 27;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAAAAA 4039

DB 26 AGGAAAAA 2

RESULT 1369

LOCUS

N52529 27 bp mRNA linear EST 15-FEB-1996

DEFINITION

YV35a12.g1 Soares fetal liver spleen INFIS Homo sapiens cDNA clone
IMAGE:244702.3 similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
HIN-1 (HUMAN); mRNA sequence.

ACCESSION

N52529 N52529.1 GI:1193695

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

FEATURES

source

Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers

1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3793948"
/db_xref="taxon:9606"
/clone="IMAGE:244702"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone="1b-Soares fetal liver spleen INFIS"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo (dt) primer
[5' AACGGAAGAATTATTAAGTCTTTTCTTTTCTTTT 3']"
double-stranded cDNA was ligated to Eco RI adapters
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

Query Match

Best Local Similarity 73.1%; Score 15.4; DB 1; Length 27;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4009 TCTAAATGAGAAAAAGAGAAAAA 4034

DB 26 TCNAAAAA 1

RESULT 1370

LOCUS

R37697 28 bp mRNA linear EST 04-MAY-1995

DEFINITION

YF50C03.g1 Soares infant brain INFIS Homo sapiens cDNA clone
IMAGE:25521.3 similar to gb:U03040 SPARC PRECURSOR (HUMAN); mRNA
sequence.

ACCESSION

R37697 R37697.1 GI:795153

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT

```

Query Match      0.2%; Score 15.4; DB 1; Length 28;
Beet Local Similarity 73.1%; Pred. Mismatches 7; Indels 0; Gaps 0;
Matches 19; Conservative 0;
/db_xref="taxon:9606"
/clone="IMAGE:25521"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_1ib="Soares infant brain 1IB"
/note="Organ: whole brain; Vector: latmid BA; Site: 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer 5',
AATCGAAGAAATTCGCCGCCAGAAATTTTTTTTTTTT 3';
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the latmid BA vector
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

Qy	4014	AATGAGAAAAAGAGAGAAAA	CAAAA	4035
Db	28	ACTGAAAAA	AAAAA	3

RESULT 1371					
CF299294	CF299294	28 bp	mRNA	linear	EST 15-AUG-2003
LOCUS					
DEFINITION	7LEAF--03.E04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza				

ACCESSION CF299294

KEYWORDS EST.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

AUTHORS

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahn B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Fax: 82 31 321 6355

```

FEATURES
source      Location/Qualifiers
1. .28

```

```

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-E04"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rise leaf plasmid cDNA library II (7LEAF)"
/notes="vector: pC4-TOPO, Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match	0.23	Score 15.4	DB 1	length 28
Best Local Similarity	76.0%	Pred. No. 1.8e+03		
Best Local 19, Conservative	0	Mismatches 6	Indels 0	Gaps 0

Qy	4012	AAAAATGAGAAAAAGAGAAAA	CA	4036
Db	2	AAAAAAAAAAAAAAAAAAAAA	CA	26

LOCUS	DEFINITION	29 bp	mRNA	linear	EST 14-OCT-2003
LOCUS BX67540					
DEFINITION BX67540	Glossina morsitans morsitans adult infected gut				
	morsitans morsitans cDNA clone Tse85f02, plc, mRNA sequence.				

ACCESSION	BX567540	GI:33434463
VERSION	BX567540.1	
KEYWORDS	EST.	

ORGANISM

REFERENCE
1 (bases 1 to 29)

AUTHORS	TITLE
Lehman, M. J., Akseoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M. B., Ronaldo, P., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N

Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lennane
Prof. M.J.Lennane
School of Biological Sciences,
University of Wales,

Bangor L157 20W
All clones with suffix q1c are reverse primer reads starting at 5' end of the CDNA all plc reads are from the 3' end.

FEATURES	Location/Qualifiers
source	1. .29

```

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sdb_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse88f02.plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
"country": Zimbabwe, EST from adult gut infected with
".brucei"

```

Query Match	0.2%	Score 15.4	DB 1	Length 29
Best Local Similarity	76.0%	Pred. No. 1.9e+03		
Matches 19; Conservative	0	Mismatches 16	Indels 0	Gaps 0

Qy	4020	AAAAAAAAAGAGAAAAACAAAATGTTA	4044
Db	28	AAAAAAAAAAAAAAAAAAAACTTTTA	4

RESULT 1373

LOCUS	CF297930	31 bp	mRNA	linear	EST_15-AUG-2003
DEFINITION	7LEAF-01-B17.g1 Rice leaf plasmid CDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF-01-B17, mRNA sequence.				

VERSION CF297930.1 GI:33669691

SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 31)

AUTHORS
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. 31

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF-01-B17"

/issue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 32;
Best Local Similarity 76.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 6;

QY 4017 GAGAAAAAGAGAAAAACAAATG 4041
DB 30 GAAAAAAGAAAAAAGAAAAAAGC 6

RESULT 1375

LOCUS CF292071/c

DEFINITION 14ROOT--02-M02.g1 Rice root plasmid cDNA library (14ROOT) Oryza

VERSION CF292071

KEYWORDS CF292071.1 GI:33661104

SOURCE EST.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 34

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-M02"

/issue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_1lb="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

Query Match 0.2%; Score 15.4; DB 1; Length 34;
Best Local Similarity 66.7%; Pred. No. 2e+03; 11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 11;

QY 3997 AAACTCTTAGCTTAAATGAGAAAAAGAA 4029
DB 34 AAATCGTTGCTCAAAAAAAGAAAAA 2

RESULT 1376

LOCUS CF310898/c

DEFINITION 14ROOT--02-M02.g1 Rice root plasmid cDNA library (14ROOT) Oryza

VERSION CF310898

KEYWORDS CF310898.1 GI:33682659

SOURCE EST.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 35)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 35

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ROOT--02-M02"

/issue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_1lb="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

library (HD) Oryza sativa cDNA clone HD-07-N06, mRNA sequence.
 CF317946
 VERSION CF317946.1 GI:33569707
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-07-N06"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDACT-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR-TOPPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 69 GCGGGCGGGCGGCGGCGGCGG 88
 |||||
 1 GCGGCGGCGGCGGCGGCGGCGG 20.

RESULT 1380
 CF319443 20 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--04-003.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa cDNA clone RCL1--04-003, mRNA sequence.
 ACCESSION CF319443
 VERSION CF319443.1 GI:33827271
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="RCL1--04-003"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SacI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SacI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURES
 source
 Location/Qualifiers
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="RCL1--04-003"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SacI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SacI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 GCGGCGGCGGCGGCGGCGGCGG 69
 |||||
 1 GCGGCGGCGGCGGCGGCGGCGG 20

RESULT 1381
 CF340627 20 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--08-K02.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa cDNA clone RCL1--08-K02, mRNA sequence.
 ACCESSION CF340627
 VERSION CF340627.1 GI:33829609
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOLOGICAL AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="RCL1--08-K02"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site_1: SacI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SacI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTT 4482
 |||||
 1 CTTTTTTTCCCTTTTTT 20

RESULT 1382
 AZ345646 20 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0080K20F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0080K20 F, genomic survey sequence.

ACCESSION AZ345646
 VERSION AZ345646
 KEYWORDS GI:10424883
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Bakkayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: K column: 20
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

1..20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0080K20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1[4732114]gb[AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4466 TTTTTTTTTTTTTTTGT 4485
 |||||
 20 TTTTTTTTAAAGTTGT 1

RESULT 1383
 AZ417235 20 bp DNA linear GSS 03-OCT-2000
 LOCUS 1M0192N15R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0192N15 R, genomic survey sequence.

ACCESSION AZ417235
 VERSION AZ417235
 KEYWORDS GI:10541248
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Bakkayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0192 row: N column: 15
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0192N15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1[4732114]gb[AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3635 GAGAGAGCTAGATGGGAA 3654

Db 20 TGCGGAGGAGGAGGAGGAA 1

RESULT 1384

AZ592714

LOCUS

DEFINITION 20 bp DNA linear GSS 13-DEC-2000

clone UGCG1M0403P13 R, genomic survey sequence.

ACCESSION AZ592714.1 GI:11714904

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0403P13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

High quality sequence stop: 20.

Location/Qualifiers

1.20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0403P13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 1.2e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

5781 TGCGTGCCTGCTGCTGCC 5800

|||||

Db 1 TGCGTGCCTGCTGCTGCTCC 20

RESULT 1385

AZ626475

LOCUS

DEFINITION 20 bp DNA linear GSS 13-DEC-2000

clone UGCG1M0466E16 R, genomic survey sequence.

ACCESSION AZ626475.1 GI:11748665

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1.20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0466E16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

High quality sequence stop: 20.

Location/Qualifiers

1.20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0466E16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UGCG1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 1.2e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

35 GCTGAGGCTCGCGGCGGC 54

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RESULT	1386
AZ468862/c	
LOCUS	AZ468862
DEFINITION	AZ468862 21 bp DNA linear GSS 04-OCT-2000
ACCESSION	U0282004 Mouse 10kb plasmid U0282004 F, genomic clone U0282004 F, genomic survey sequence.
VERSION	AZ468862
KEYWORDS	AZ468862.1 GI:10626987
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
TITLE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isaiam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

FEATURES	High quality sequence stop: 21.
source	Location/Qualifiers
	1. .21

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08100282004"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U08100282004 library"
 /note="Vector: pMD24env; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD24 (g1147311[g]A123072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

	Query Match	Similarity	Score	DB	Length
Oy	Best Local	85.0%	15.2	1	21
db	Matches	17	Conservative	0	Mismatches 3, Indels 0, Gaps 0
	2996	GTCCCCACCCCTCACCCCA	3015		
	21	GAACCCCAACCCCAACCCCA	2		

RESULT	1387
LOCUS	A2625662/c
DEFINITION	21 bp DNA linear GSS 13-DEC-2000 M0465C23F Mouse 10kb plasmid UUGCM library Mus musculus genomic clone UUGCM0465C23 F, genomic survey sequence.
ACCESSION	A2625662
VERSION	A2625662
KEYWORDS	A2625662.1 GI:11747852
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
JOURNAL COMMENT	Contact: Robert B. Weiss

FEATURES	Location/Qualifiers
SOURCE	1. .21

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C1M0465C23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid U08C1M library"
 /note="Vector: PWD242v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 [gi|47321419|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

```

Query Match      0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      4464 TTTT TTTT TTTT TTTT TTTT TTTT 4463
      | | | | | | | | | | | | | | | | | |
Db      21 TATATATATATATATATATATATATATATAT 2

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RESULT 1388
TA36E110/C 21 bp DNA linear GSS 13-DEC-2000
LOCUS T. Brucei sheared genomic DNA clone 36e11, reverse sequence.
DEFINITION
ACCESSION AL454378
VERSION AL454378.1 GI:11855182
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 21)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct SubMISSION
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhs@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Detail of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..21
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="36e11"

Query Match 0.2%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5909 CTGTTCCCAAGCCAGAGA 5928
DB 20 CTGTTCCCAAGTCAGAGA 1

RESULT 1389
A2854229/C 22 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0157C14R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION
ACCESSION A2854229
VERSION A2854229.1 GI:13043139
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetice.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0157 row: C column: 14
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES
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/mol_type="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0157C14"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5316 TTCCTCTCTTCTCTCTTT 5335
DB 21 TTTTCTCTTCTCTCTTT 2

RESULT 1390
A2470212 22 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0284L09F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION
ACCESSION A2470212
VERSION A2470212.1 GI:10628337
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

```

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0284 row: L column: 09
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Source

1. .22
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0284L09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[473214]gb[AP129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4459 TGGACTTTTCTTTTCTTTT 4478
Db 2 TGGCTTTCTTTTCTTTTCTTTT 21

RESULT 1391
A2875902/c 22 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION 2M0190K12R Mouse 10kb plasmid U08C1M library Mus musculus genomic
ACCESSION A2875902
VERSION A2875902.1 GI:13086357
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: K column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

Source

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[473214]gb[AP129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 3624 GGTGGGGTGGGAGAGAGAG 3643
Db 22 GGGGGGGGGGGAGAGCGG 3

RESULT 1392
AL587602/c 23 bp mRNA linear EST 02-MAR-2001
LOCUS
DEFINITION AL587602 BP Chicken Brain Library Gallus gallus cdna clone
ACCESSION R08059F08, mRNA sequence.
VERSION AL587602
KEYWORDS EST.

SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 23)
AUTHORS Archibutea, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

TITLE Unpublished (2001)
JOURNAL BP Chicken Brain Library
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GGGCGCGCTTTTCTTTTCTTTT 3 Poly A RNA purchased from Clontech (*6854-

Seq primer: M13F.

FEATURES
Location/Qualifiers

```

1..23
/organism="Gallus gallus"
/mol_type="rRNA"
/db_xref="taxon:9031"
/clone="ROS059F08"
/tissue_type="Brain"
/dev_stage="unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTGAG 3'; 3' adaptor sequence: 5'
CGGCGCCCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
Clontech (#6854-1)"

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Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 81.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4012 AAATGAGAGAGAGAGAA 4032
 |||||
 Db 23 AAAAAAAAAAAAAAAAAAGAA 3

RESULT 1393

AZ308643 23 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0011013R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0011013 R, genomic survey sequence.

ACCESSION AZ308643
 VERSION AZ308643.1 GI:10348845
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

REFERENCE

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center

TITLE

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0011 row: O column: 13
 Seq primer: CACACAGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES
source

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1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0011013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114[9b]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 23;
 Best Local Similarity 85.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4604 TTCTGCCCCACTGCTTGGG 4623
 |||||
 Db 1 TTCTCACCACCACTGCTTG 20

RESULT 1394

AZ345908 23 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0080F22R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0080F22 R, genomic survey sequence.

ACCESSION AZ345908
 VERSION AZ345908.1 GI:10425145
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

REFERENCE

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center

TITLE

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: F column: 22
 Seq primer: CACACAGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES
source

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1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0080F22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[14732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5473 TTTTGTGTAAGATATAT 5492
Db 22 TTTGTTGTAAGATATAT 3

RESULT 1395
LOCUS AZ468097 23 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0279K22R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0279K22 R, genomic survey sequence.

ACCESSION AZ468097
VERSION AZ468097.1 GI:10626222
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0279 row: K column: 22
Seq primer: CACACAGAAACACCTATGAC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0279K22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g[14732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTTGTTGTTT 4483
Db 4 TTTTGTGTTGTTGTTT 23

RESULT 1396
LOCUS AZ970753 23 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0244E01F Mouse 10kb plasmid UGCM2M library Mus musculus genomic
clone UGCM2M0244E01 F, genomic survey sequence.

ACCESSION AZ970753
VERSION AZ970753.1 GI:13841980
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: E column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM2M0244E01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM2M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2% Score 15.2; DB 1; Length 23;
Best Local Similarity 85.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2877 GGAGCTGGGCTGAGGAGAG 2896
Db 3 GGAGCTGGGCTGAGGAGGCTG 22

RESULT 1397
A2437459/c 26 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION 1M0225B15R Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION A2437459
VERSION A2437459.1 GI:10561472
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 26)
Mammalia; Eutheria; Rodentia; Sclitognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niedermauern, A. and Wright, D., Weiss, R.

TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 15
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0225B15"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2% Score 15.2; DB 1; Length 26;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4020 AAAAAAGAGAAACAA 4039
Db 25 AAAAAAAAGAAAAAGAAA 6

RESULT 1398
AM332443 28 bp mRNA linear EST 31-JAN-2000
LOCUS
DEFINITION S8E7 AGS-1 Pneumocystis carinii CDNA 3', mRNA sequence.
ACCESSION AM332443
VERSION AM332443.1 GI:6828800
KEYWORDS EST.
SOURCE Pneumocystis carinii
ORGANISM Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;

REFERENCE
AUTHORS
1 (bases 1 to 28)
Smilian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
Edman, J.C., Kovacs, J. and Cushion, M.
Expressed sequence tags from *Pneumocystis carinii*
Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: stabenpop.uky.edu.

FEATURES

source
1..28
Location/Qualifiers
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_1lb="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Tritol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.2% Score 15.2; DB 1; Length 28;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 4012 AAAAAAGAGAAACAA 4039
Db 28 AAAAAAAATAAAAAAAGAAAA 1

RESULT 1399
TA327D04P/c 28 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION TA327D04P
T. brucei sheared genomic DNA clone 327D04, forward sequence,
genomic survey sequence.

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ACCESSION      AL497297      GI:11867974
VERSION        GSS.
KEYWORDS       Trypanosoma brucei
SOURCE         Trypanosoma brucei
ORGANISM       Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
               Chillingworth, C., Ormond, D., Harrie, B., El-Sayed, N., Hou, L.,
               Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE          Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
JOURNAL        Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES       Location/Qualifiers
               1..28
               /organism="Trypanosoma brucei"
               /mol_type="genomic DNA"
               /strain="TRBU927"
               /db_xref="taxon:5691"
               /clone="327d04"

Query Match      0.2%; Score 15.2; DB 1; Length 28;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      3271 TTGTGTTAAGAGAAATGAAACGACA 3298
          |||||
          28 TTTTAAATMAAAAAAAAAAAAAA 1

RESULT 1400
CF314795/c     29 bp      mRNA      linear      EST 15-AUG-2003
LOCUS          HD-03-H09.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
ACCESSION      CF314795
VERSION        CF314795.1
KEYWORDS       GI:33686556
SOURCE         EST.
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzaceae; Oryza.
               1 (bases 1 to 29)
REFERENCE      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
               Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
               Large-scale Sequencing Analysis of Rice ESTs
               Unpublished (2003)
               Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc., Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
               Location/Qualifiers
               1..29
               /organism="Oryza sativa"

```

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--03-H09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

QY      3271 TTGTGTTAAGAGAAATGAAACGACA 3298
          |||||
          29 TTTTAAATMAAAAAAAAAAAAAA 2

Query Match      0.2%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      3271 TTGTGTTAAGAGAAATGAAACGACA 3298
          |||||
          29 TTTTAAATMAAAAAAAAAAAAAA 2

RESULT 1401
BQ586486       29 bp      mRNA      linear      EST 06-DEC-2002
LOCUS          BQ12391-024-012-J22-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION     024-012-J22 5-PRIME, mRNA sequence.
ACCESSION      BQ586486
VERSION        BQ586486.1
KEYWORDS       GI:26116068
SOURCE         EST.
ORGANISM       Beta vulgaris
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Caryophyllales; Amaranthaceae; Beta.
               1 (bases 1 to 29)
REFERENCE      Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinbach, M.,
               Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehmach, H.
               and Kadetot, U.
               Construction of a 'unigene' cDNA clone set by oligonucleotide
               fingerprinting allows access to 25 000 potential sugar beet genes
               Plant J. 32 (5), 845-857 (2002)
JOURNAL        MEDLINE
MEDLINE        22362189
PUBMED         12472698
COMMENT        Contact: Weisshaar B
               ADIS DNA core facility at MP12
               Max-Planck-Institute for Plant Breeding Research
               Carl-von-Linne Weg 10, 50829 Koeln, Germany
               Fax: 00492215062851
               Email: weisshaar@mp12-koeln.mpg.de
               Insert Length: 29      Std Error: 0.00
               Plate: 12      Row: 1      Column: 22
               Seq primer: SP6; CATACGATTGCTGACACTATAG.
               Location/Qualifiers
               1..29
               /organism="Beta vulgaris"
               /mol_type="mRNA"
               /cultivar="KWS2320 (double haploid, monogerm breeding
               line)"
               /db_xref="GABI:186373"
               /db_xref="taxon:161934"
               /clone="024-012-J22"
               /tissue_type="leaf"
               /lab_host="EMDH10B"
               /clone_lib="MP12-ADIS-024-leaf"
               /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
               cDNA library from sugar beet. Library provided by KWS
               Kleinfelderleber Saatzucht AG Binbeck, Germany, contact:
               b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
               orientation:
               SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-TI; Note:

```

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 15.2; DB 1; Length 29;
 Best Local Similarity 71.4%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6964 GAGGAAATGAGCTAATAACCAACGAA 6991
 Db 1 GAAAGAGAGACCAAAAAAAAAAAAAA 28

RESULT 1402
 LOCUS CF312595/c 29 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--08-G19-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-G19, mRNA sequence.
 ACCESSION CF312595
 VERSION CF312595.1 GI:33684356
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..29
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--08-G19"
 /cissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_id="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: PCR4-TOPO, site_1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABF-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15.2; DB 1; Length 29;
 Best Local Similarity 71.4%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGGAGAAACAAATGT 4042
 Db 29 ATAAAAAAAAAAAAAAAAAACTGT 2

RESULT 1403
 LOCUS TA378G07P/c 29 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 378G07, forward sequence.
 ACCESSION AL497621
 VERSION AL497621.1 GI:11873343

KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 29)
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Omond,P., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrall,B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrall, Oxford University Press, 1999).
 Email: neilsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source Location/Qualifiers
 1..29
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="378G07"

Query Match 0.2%; Score 15.2; DB 1; Length 29;
 Best Local Similarity 71.4%; Pred. No. 2e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3271 TTGTGTTAAGAGAAATGAACCCAGA 3298
 Db 29 TTTTAAAAAATAAAAAAAAAAAAAA 2

RESULT 1404
 LOCUS CF336137/c 29 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--06-B10-g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-B10, mRNA sequence.
 ACCESSION CF336137
 VERSION CF336137.1 GI:33820654
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs unpublished (2003)
 JOURNAL Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..29
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"

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/db xref="taxon:4530"
/clone="JMT--06-B10"
/tissue type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOP0; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonic Carbonyl
methyltransferase overexpression line."

Query Match      0.2%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      4018 AGAAAAAGAGAGAAAACAAATGTTAT 4045
Db      29 AAAAAAAAAAAAAAAAAACACTGTCTAT 2

RESULT 1405
AZ962183      30 bp DNA linear GSS 27-APR-2001
LOCUS      2M0230124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION      clone UUGC2M0230124 R, genomic survey sequence.
ACCESSION      AZ962183
VERSION      AZ962183.1 GI:13833410
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: 1 column: 24
Seq primer: CACACAGAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0230124"
/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-."
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

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adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 15.2; DB 1; Length 30;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      4014 AATGAGAAAAAGAGAGAAAACAAATG 4041
Db      1 AAAAAAAAAAAAAAAAAAGG 28

RESULT 1406
AU268044      31 bp mRNA linear EST 10-MAY-2002
LOCUS      AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
DEFINITION      sequence.
ACCESSION      AU268044
VERSION      AU268044.1 GI:20526842
KEYWORDS      EST.
SOURCE      Dictyostelium discoideum
ORGANISM      Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
1 (bases 1 to 31)
Unruhshara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeruchi,I., Kohara,Y. and Tanaka,Y.
Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
Unpublished (2002)
Contact: Hideko Unruhshara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
1..31
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH836"
/sex="mat A"
/dev stage="vegetative"
/clone_lib="V5"

Query Match      0.2%; Score 15.2; DB 1; Length 31;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      4012 AAAATGAGAAAAAGAGAGAAAACAAA 4039
Db      2 AAAAAAAAAAAAAAAAAATTAATAAAAAA 29

RESULT 1407
BG501238      32 bp mRNA linear EST 27-MAR-2001
LOCUS      BG501238 602547802F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4670136 5',
DEFINITION      mRNA sequence.
ACCESSION      BG501238
VERSION      BG501238.1 GI:13462755
KEYWORDS      EST.
SOURCE      Homo sapiens (human)

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[illegible]

www.bio.llnl.gov/bbcp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center <http://www.genome.washington.edu> Low Quality Sequence: 32 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 32 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L1C6 row: G column: 3
High quality sequence stop: 32.
Location/Qualifiers

1..32

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_xref="IMAGE:2821274"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="MDH10B (phage-resistant)"
/clone_lib="NTH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." ."

Query Match
Best Local Similarity 71.4%; Pred. No.2.le+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0

OY 4012 AAATGAGAAAAAAGAGAAACAAA 4039
Dd 29 AAAAAAAAAAAAAATCAAAAAAAAAA 2

RESULT 1409
CEP279813/c
LOCUS
DEFINITION
ORFYa sativa cDNA clone 14ETL--06-E02, mRNA sequence.
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Klm,J.S., Jun,K.M., Cheung,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers
1..32
/organism="Oryza sativa"
/mol_type="mRNA"
/culivar="Naekdong"
/db_xref="taxon:4530"

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/clone="14ETL--06-E02"
/issue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      0.2%; Score 15.2; DB 1; Length 32;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      4018 AGAAAAAGAGAAAACAAATGTTAT 4045
Db      31 AAAAAAAAAAAAAAAAAACCTGCTAT 4

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```

RESULT 1410      32 bp  mRNA  linear  EST 10-OCT-2003
BX558102/c      BX558102 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION      morsitans morsitans cDNA clone Tse36f08_p1c, mRNA sequence.
ACCESSION      BX558102
VERSION      BX558102.1 GI:33429249
KEYWORDS      EST.
SOURCE      Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 32)
Lehane, M.J., Aksoy, S., Gibson, W., Kermorou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

```

```

REFERENCE
AUTHORS
TITLE
COMMENT
JOURNAL
MEDLINE
PUBMED
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse36f08_p1c"
/issue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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FEATURES
SOURCE
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse36f08_p1c"
/issue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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Query Match      0.2%; Score 15.2; DB 1; Length 32;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      4020 AAAAAAGAGAAAACAAATGTTATTT 4047
Db      32 AAAAAAAAAAAAAAAAAACTATCT 5

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RESULT 1411      32 bp  mRNA  linear  EST 10-OCT-2003
BX560723/c      BX560723 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION      morsitans morsitans cDNA clone Tse50g08_p1c, mRNA sequence.
ACCESSION      BX560723
VERSION      BX560723.1 GI:33369704
KEYWORDS      EST.
SOURCE      Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 32)
Lehane, M.J., Aksoy, S., Gibson, W., Kermorou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

```

```

REFERENCE
AUTHORS
TITLE
COMMENT
JOURNAL
MEDLINE
PUBMED
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse50g08_p1c"
/issue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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FEATURES
SOURCE
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse50g08_p1c"
/issue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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Query Match      0.2%; Score 15.2; DB 1; Length 32;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY      4020 AAAAAAGAGAAAACAAATGTTATTT 4047
Db      32 AAAAAAAAAAAAAAAAAACTATCT 5

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RESULT 1412      32 bp  mRNA  linear  EST 10-OCT-2003
BX564047/c      BX564047 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION      morsitans morsitans cDNA clone Tse50g08_p1c, mRNA sequence.
ACCESSION      BX564047
VERSION      BX564047.1 GI:33431246
KEYWORDS      EST.
SOURCE      Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hypoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 32)
Lehane, M.J., Aksoy, S., Gibson, W., Kermorou, A., Berriman, M.,

```

```

REFERENCE
AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Kermorou, A., Berriman, M.,

```



```

TITLE
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

FEATURES
Source
location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse6d04_p1c"
/tissue_type="adult infected gut"
/clone_id="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Beet Local Similarity 0.2%; Score 15.2; DB 1; Length 32;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4020 AAAAAAGCAGAAACAAATGTTATT 4047
Db 32 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1413
LOCUS BX559212/c 33 bp mRNA linear EST 10-OCT-2003
DEFINITION BX559212 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse42c04_p1c, mRNA sequence.
ACCESSION BX559212
VERSION BX559212.1 GI:33366526
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 33)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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JOURNAL
MEDLINE
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COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
All clones with suffix q1c are reverse primer reads starting at 5'

```

```

end of the cDNA all pic reads are from
the 3' end.
1.1. Location/Qualifiers
1.33
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/db_xref="taxon:37546"
/clone="1se42c04_pic"
/tissue_type="adult infected gut"
/clone_id="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4020 AAAAAAGAGAGAAAAAATGTTATTT 4047
||||| ||||| ||||| |||||
32 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1414
BE230585/c
LOCUS BE230585
DEFINITION 15 bp mRNA linear EST 07-JUN-2000
99AS799 Rice Seedling lambda ZAPII cDNA library Oryza sativa
(indica cultivar-group) cDNA clone 99AS799, mRNA sequence.
ACCESSION BE230585
VERSION BE230585.1 GI:8956782
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphorbiales; Magnoliophyta; Liliopsida; Poales; Poaceae;
Echinozoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
Nam,W.B.H.
Large-scale Sequencing Analysis of ESTs from Rice Seedling
unpublished (1999)
Contact: Eun M.Y.
Department of Cyto genetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sunn20.asst.re.kr.
Location/Qualifiers
1.15
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/clone_id="Rice Seedling lambda ZAPII cDNA library"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site"

Query Match 0.23; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTTTTTTTTTTTT 4478
||||| ||||| ||||| |||||
15 TTTTTTTTTTTTTT 1

RESULT 1415

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B0582543 15 bp mRNA linear EST 06-DEC-2002
 LOCUS B0582543
 DEFINITION S013300-024-007-B02-T7 MP12-ADIS-024-inflorescence Beta vulgaris
 ACCESSION B0582543
 VERSION B0582543.1 GI:26112120
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 15 Std Error: 0.00
 Plate: 7 row: B column: 02
 Seq primer: T7; GTATACGCTGACTATATAGGC.
 Location/Qualifiers
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 /cultiVar="KMS2320 (double haploid, monogerm breeding
 line)"
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 /db_xref="taxon:161934"
 /clone="024-007-B02"
 /issue_type="inflorescence"
 /lab_host="EMDH10B"
 /clone_1lb="MP12-ADIS-024-inflorescence"
 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KMS
 Kleimanzlebener Saatzzucht AG Binbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1416
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 LOCUS B0585820
 DEFINITION E012533-024-014-H17-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
 024-014-H17 5-PRIME, mRNA sequence.
 ACCESSION B0585820
 VERSION B0585820.1 GI:26115402
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 15 Std Error: 0.00
 Plate: 14 row: H column: 17
 Seq primer: SP6; CATACGATTTAGCTGACACTATAG.
 Location/Qualifiers
 1..15
 /organism="Beta vulgaris"
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 line)"
 /db_xref="GABI:187164"
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 /issue_type="leaf"
 /lab_host="EMDH10B"
 /clone_1lb="MP12-ADIS-024-leaf"
 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KMS
 Kleimanzlebener Saatzzucht AG Binbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1417
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 LOCUS B0590410
 DEFINITION E012844-024-019-M08-T7 MP12-ADIS-024-storage root Beta vulgaris
 cDNA clone 024-019-M08 3-PRIME, mRNA sequence.
 ACCESSION B0590410
 VERSION B0590410.1 GI:26119993
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189

PUBMED 12472698
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpi-z-koeln.mpg.de
 Insert Length: 15 Std Error: 0.00
 Plates: 19 row: M column: 08
 Seq primer: T7; GTAATTCAGCTCACTATAGGCG.
 Location/Qualifiers
 1. 15
 /organism="Beta vulgaris"
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 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polys-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTT 4478
 Db 1 TTTTTTTTTTTTTT 15

RESULT 1418
 BOS90656 15 bp mRNA linear EST 06-DEC-2002
 LOCUS
 DEFINITION CDNA clone 024-018-L13-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
 ACCESSION BOS90656
 VERSION BOS90656.1 GI:26120239
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 15)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpi-z-koeln.mpg.de
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 Plates: 18 row: L column: 13
 Seq primer: SP6; CATAGATTTAGTGACACTATAG.

FEATURES
 source Location/Qualifiers
 1. 15
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 /issue_type="storage root"
 /lab_host="EMDH108"
 /clone_1lb="MPIZ-ADIS-024-storage root"
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polys-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTT 4478
 Db 1 TTTTTTTTTTTTTT 15

RESULT 1419
 BOS91170 15 bp mRNA linear EST 06-DEC-2002
 LOCUS
 DEFINITION E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-017-N18 3-PRIME, mRNA sequence.

ACCESSION BOS91170
 VERSION BOS91170.1 GI:26120753
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 15)
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpi-z-koeln.mpg.de
 Insert Length: 15 Std Error: 0.00
 Plates: 17 row: N column: 18
 Seq primer: T7; GTAATTCAGCTCACTATAGGCG.
 Location/Qualifiers
 1. 15
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 /db_xref="taxon:161934"
 /clone="024-017-N18"
 /issue_type="storage root"

/lab host="EMDH10B"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatzzucht AG Bindeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1420
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LOCUS E012715-024-017-F22-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-F22 3-PRIME, mRNA sequence.
ACCESSION BQ591178
VERSION BQ591178.1 GI:26120761
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PubMed 12472698

COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: F column: 22
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
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/issue_type="storage root"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatzzucht AG Bindeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

FEATURES
source

Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
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RESULT 1421
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LOCUS E012715-024-017-H02-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-H02 3-PRIME, mRNA sequence.
ACCESSION BQ591223
VERSION BQ591223.1 GI:26120806
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
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JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
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COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 17 row: H column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. 15
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line)"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatzzucht AG Bindeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

FEATURES
source

RESULT 1422
BOS94689 15 bp mRNA linear EST 06-DEC-2002
LOCUS E012404-024-024-M05-T7 MP1Z-ADIS-024-developing root Beta vulgaris
DEFINITION cDNA clone 024-024-M05-3-PRIME, mRNA sequence.
ACCESSION BOS94689
VERSION BOS94689.1 GI:26124272
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
Hwang, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehmach, H. and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE 12472698
PUBMED
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 15 Std Error: 0.00
Plate: 24 row: M column: 05
Seq primer: T7; GTPATACGACCTCATATAGGC.
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:161934"
/clone="024-024-M05"
/issue_type="developing root"
/lab_host="EMDH108"
/clone_1ib="MP1Z-ADIS-024-developing root"
/note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatgut AG Sinbeck, Germany, contact: b.schulz@kwa.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sall-CCACGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BeeT project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"
Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1423
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LOCUS CF277319
DEFINITION 14ETL--02-M23-b1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF277319
VERSION CF277319.1 GI:33654705
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1424
CF281923 15 bp mRNA linear EST 14-AUG-2003
LOCUS CF281923
DEFINITION 14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF281923
VERSION CF281923.1 GI:33659310
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
JOURNAL Unpublished (2003)
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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .15
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/clone="14ETL--09-D04"
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Best Local Similarity 100.0%; Pred. No. 6.9e+02;
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Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1425

CF290920 15 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-C09.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION bactiva cDNA clone 14ROOT--01-C09, mRNA sequence.
ACCESSION CF290920
VERSION CF290920.1 GI:33659953
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE location/Qualifiers
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1426
CF291029 15 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION bactiva cDNA clone 14ROOT--01-E19, mRNA sequence.

ACCESSION CF291029
VERSION CF291029.1 GI:33660062
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
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Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source location/Qualifiers
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1427

CF291103 15 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION bactiva cDNA clone 14ROOT--01-G10, mRNA sequence.
ACCESSION CF291103
VERSION CF291103.1 GI:33660136
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source location/Qualifiers
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/cultivar="Nackdong"
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
1 TTTT TTTT TTTT TTTT 15

RESULT 1428

LOCUS CF291717 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-E04.b1 Rice root plasmid cDNA library (14ROOT) Oryza
ACCESSION CF291717
VERSION CF291717.1 GI:33660750
KEYWORDS EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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Qy 4464 TTTT TTTT TTTT TTTT 4478
1 TTTT TTTT TTTT TTTT 15

RESULT 1429

LOCUS CF291798 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-G02.b1 Rice root plasmid cDNA library (14ROOT) Oryza

sativa cDNA clone 14ROOT--02-G02, mRNA sequence.

ACCESSION CF291798
VERSION CF291798.1 GI:33660831
KEYWORDS EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

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of Bioscience and Bioinformatics, Myongji University
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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
1 TTTT TTTT TTTT TTTT 15

RESULT 1430

LOCUS CF292458 15 bp mRNA linear EST 14-AUG-2003
DEFINITION 30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
ACCESSION CF292458
VERSION CF292458.1 GI:33661491
KEYWORDS EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

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with oligoribonucleotides and then used as templates for
RT-PCR."

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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1431

CF292461 15 bp mRNA linear EST 14-AUG-2003
 LOCUS 30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 DEFINITION sativa cDNA clone 30DGS--01-E19, mRNA sequence.

ACCESSION CF292461
 VERSION CF292461.1 GI:33661494
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriactroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

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 of Bioscience and Bioinformatics, Myongji University

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

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RT-PCR."

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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1432

CF296652 15 bp mRNA linear EST 14-AUG-2003
 LOCUS CF296652

DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 sativa cDNA clone 30DGS--07-C02, mRNA sequence.

ACCESSION CF296652

VERSION CF296652.1 GI:33665685

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriactroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

CONTACT: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

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RT-PCR."

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QY 4470 TTTT TTTT TTTT TTTT TTTT 4484
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1433

CF298148 15 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--01-G17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa cDNA clone 7LEAF--01-G17, mRNA sequence.

ACCESSION CF298148

VERSION CF298148.1 GI:33669909

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriactroideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

CONTACT: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

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Query Match 0.2%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1434
CF298630 15 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-B23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-B23, mRNA sequence.
ACCESSION CF298630
VERSION CF298630.1 GI:33670391
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 15

FEATURES
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Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1435
CF298733

LOCUS CF298733 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION sativa cDNA clone 7LEAF--02-E20, mRNA sequence.
CF298733
VERSION CF298733.1 GI:33670494
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyonggi, Korea
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
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FEATURES
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/clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4478
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1436
CF298805 15 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-G20, mRNA sequence.
ACCESSION CF298805
VERSION CF298805.1 GI:33670566
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 15

FEATURES
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1. 15
/organism="Oryza sativa"
/mol_type="mRNA"
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/issue_type="leaf"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1435
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1437

CF298889 15 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-J09, mRNA sequence.
ACCESSION CF298889
VERSION CF298889.1 GI:33670650
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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1. .15
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/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1438

CF299602 15 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L01, mRNA sequence.
ACCESSION CF299602
VERSION CF299602.1 GI:33671363
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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1. .15
/organism="Oryza sativa"
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1439

CF299608 15 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-L04, mRNA sequence.
ACCESSION CF299608
VERSION CF299608.1 GI:33671369
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. .15
/organism="Oryza sativa"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1439

FEATURES

source

Location/Qualifiers
1. .15
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1440

CF300121

LOCUS 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF300121
VERSION CF300121
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Fax: 82 31 321 6355
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. .15
Location/Qualifiers

/organism="Oryza sativa"
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Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1441

CF300361

LOCUS 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF300361
VERSION CF300361
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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of Bioscience and Bioinformatics, Myongji University
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Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. .15
Location/Qualifiers

/organism="Oryza sativa"
/mol_type="mRNA"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1442

CF300992

LOCUS 15 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF300992
VERSION CF300992
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

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1..15
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1443

CEP302034 15 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--07-C24, mRNA sequence.

ACCESSION CEP302034

VERSION CEP302034.1 GI:33673795

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..15

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--07-C24"

/tissue_type="leaf"

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/clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1444

CEP302124

LOCUS 7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--07-F16, mRNA sequence.

ACCESSION CEP302124

VERSION CEP302124.1 GI:33673885

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..15

/organism="Oryza sativa"

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with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1445

CEP302182 15 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--07-H20, mRNA sequence.

ACCESSION CEP302182

VERSION CEP302182.1 GI:33673943

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Location/Qualifiers

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/organism="Oryza sativa"

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/clone_1ib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT TTTT 15

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Location/Qualifiers

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source 1.15

/organism="Oryza sativa"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1446

LOCUS CF307923 15 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-115.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-115, mRNA sequence.
ACCESSION CF307923
VERSION CF307923.1 GI:33679684
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

JOURNAL
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Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

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1.15
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1447

LOCUS CF311159 15 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.
ACCESSION CF311159
VERSION CF311159.1 GI:33682920
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1.15
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/mol_type="mRNA"
/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1448

LOCUS CF311907 15 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.
ACCESSION CF311907
VERSION CF311907.1 GI:33683668
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
JOURNAL
COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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cDNA library (ABF)"

/note="vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

4464 TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1449

CF313319

LOCUS HD--01-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

DEFINITION 15 bp mRNA linear EST 15-AUG-2003

ACCESSION CF313319

VERSION CF313319.1 GI:33685080

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

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/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
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/note="vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

4464 TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1450

CF313320/c

LOCUS HD--01-G13.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

DEFINITION 15 bp mRNA linear EST 15-AUG-2003

ACCESSION CF313320

VERSION CF313320.1 GI:33685081

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

/mol_type="mRNA"

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/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"

/note="vector: pCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4478

Db 15 TTTT TTTT TTTT TTTT 1

RESULT 1451

CF316251/c

LOCUS HD--05-H15.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

DEFINITION 15 bp mRNA linear EST 15-AUG-2003

ACCESSION CF316251

library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.


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VERSION CF316251.1 GI:33688012
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacroidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
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/organism="Oryza sativa"
/mol_type="mRNA"
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/clone="HD--07-P06"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 15 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1452
CF318035 15 bp mRNA linear EST 15-AUG-2003
LOCUS HD--07-P06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.
ACCESSION CF318035
VERSION CF318035.1 GI:33689796
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacroidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..15

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/organism="Oryza sativa"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1453
CF327434 15 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--01-018.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--01-018, mRNA sequence.
ACCESSION CF327434
VERSION CF327434.1 GI:33803127
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacroidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4478
Db 1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 1454
CF330195          15 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION      NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION      CF330195
VERSION        CF330195
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.
                Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1..15
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/lab_host="E.coli DH10B"
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 15; DB 1; Length 15;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1455
CF330668          15 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION      NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION      CF330668
VERSION        CF330668
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.
                Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
SOURCE
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

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/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1456
CF332178          15 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION      NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION      CF332178
VERSION        CF332178
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
                Contact: Nahm B.H.
                Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
                Location/Qualifiers

FEATURES
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1..15
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
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Query Match      0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT 4478
Db      1 TTTT TTTT TTTT TTTT TTTT 15

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RESULT 1457
CF336202
LOCUS
DEFINITION CF336202 15 bp mRNA linear EST 16-AUG-2003
JMT--06-C20.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.
ACCESSION CF336202
VERSION CF336202.1 GI:33820794
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridaceae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 15
/organism="Oryza sativa"
/mol_type="mRNA"
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/issue_type="leaf"
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cDNA library (JMT)"
/note="Vector: PCR-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478
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1 TTTT TTTT TTTT TTTT 15

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1458
BOS90507
LOCUS
DEFINITION BOS90507 16 bp mRNA linear EST 06-DEC-2002
E01844-024-019-M04-T7 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION BOS90507
VERSION BOS90507.1 GI:26120090
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hemmig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189
PubMed 12472698
COMMENT
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp12-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: T7; GTAATACGACCTCATTAGGCG.
Location/Qualifiers
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line)"
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/clone="024-019-M04"
/issue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/note="Vector: PCWVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5Prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 15

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1459
BOS95369
LOCUS
DEFINITION BOS95369 16 bp mRNA linear EST 06-DEC-2002
S013317-024-022-P02-T7 MP12-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION BOS95369
VERSION BOS95369.1 GI:26124952
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hemmig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 12472698
PubMed 12472698
COMMENT
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp12-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: P column: 02

Seq primer: T7; GATATGACTCACTATAGGCG.
 location/Qualifiers

1. .16
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiVar="KMS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:191489"
 /db_xref="taxon:161934"
 /clone="024-022-P02"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_1lb="MP12-ADIS-024-developing root"
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleimanzlebener Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1460
 CF3296130

LOCUS CF3296130 16 bp mRNA linear EST 14-AUG-2003
 DEFINITION batiVa cDNA clone 30DGS--06-F22, mRNA sequence.
 ACCESSION CF3296130
 VERSION CF3296130.1 GI:33665163
 KEYWORDS EST.

SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 SOURCE

1. .16
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultiVar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--06-F22"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1461
 CF314013

LOCUS CF314013 16 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD-02-G01.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD-02-G01, mRNA sequence.
 ACCESSION CF314013
 VERSION CF314013.1 GI:33685774
 KEYWORDS EST.

SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 16)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
 YONGIN, KYEONGGI, KOREA
 TEL: 82 31 330 6193
 FAX: 82 31 321 6355
 EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 SOURCE

1. .16
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultiVar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-02-G01"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_1lb="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4478
 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 1462
 CF329320

LOCUS CF329320 16 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--04-J17, mRNA sequence.
 ACCESSION CF329320
 VERSION CF329320.1 GI:33806877
 KEYWORDS EST.

SOURCE
 ORGANISM

Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 16)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

1..16 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultiivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--04-J17"
 /issue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1463

CF311499

LOCUS CF311499 17 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.

ACCESSION

CF311499

VERSION CF311499.1 GI:33683260

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacoidae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 17)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

1..17 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultiivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--06-L20"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.2%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1464

CF298591

LOCUS CF298591 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--02-A20, mRNA sequence.

ACCESSION

CF298591

VERSION CF298591.1 GI:33670352

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacoidae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 18)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

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 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 18;
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4478
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1465

CF301359

LOCUS CF301359 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--06-D05, mRNA sequence.

ACCESSION

CF301359

VERSION CF301359.1 GI:33673120

KEYWORDS

EST.

SOURCE	Oryza sativa
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES	location/Qualifiers 1..18 /organism="Oryza sativa" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:4530" /clone="7LEAF--06-D05" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="vector: PCR4-TOPO; site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
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Best Local Similarity	100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	4464 TTTT TTTT TTTT TTTT 4478 1 TTTT TTTT TTTT 15
Db	
RESULT 1466	
LOCUS	CF309376 18 bp mRNA EST 15-AUG-2003
DEFINITION	ABF--03-119.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-119, mRNA sequence.
ACCESSION	CF309376
VERSION	CF309376.1 GI:33681137
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.	
large-scale Sequencing Analysis of Rice ESTs	
Unpublished (2003)	
Contact: Nahm B.H.	
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University	
Yongin, Kyeonggi, Korea	
Tel: 82 31 330 6193	
Fax: 82 31 321 6355	
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.	
location/Qualifiers	
1..18	
/organism="Oryza sativa"	
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/cultivar="Nackdong"	
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/clone="ABF--03-119"	

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Query Match          0.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 TTTTTTTTTTTTTTTT 15

RESULT 1467
LOCUS    CF329484                      18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329484
VERSION   CF329484.1 GI:33807207
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.,
TITLE       Large-scale Sequencing Analysis of Rice Ests
COMMENT     Unpublished (2003)
JOURNAL    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myoungji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnah@ggbio.com, bhnahmbio.myongji.ac.kr.
FEATURES             location/Qualifiers
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                 /tissue_type="callus"
                 /dev_stage="proliferated callus on 2N6 media for 30 days"
                 /lab_host="E.coli DH10B"
                 /clone_id="Rice callus plasmid cDNA library (NACL)"
                 /note="Vector: PCR4-TOPo; Site 1: EcoRI; mRNA was capped
                   with oligoribonucleotides and then used as templates for
                   RT-PCR."

Query Match          0.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTTTTTTTTTTTTTT 4478
         |||||
Db       1 TTTTTTTTTTTTTTTT 15

RESULT 1468
LOCUS    CF329485                      18 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza
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active cDNA clone NACL-04-N06, mRNA sequence.

CF329495
VERSION
CF329485.1 GI:33807209

KEYWORDS
EST.

SOURCE
Oryza sativa

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
Unpublished (2003)

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL-04-N06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred.No.1e+03; Length 18;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 18 TTTT TTTT TTTT TTTT TTTT 4

RESULT 1469

CF278272 19 bp mRNA linear EST 14-AUG-2003

LOCUS 14ETL-04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)

DEFINITION Oryza sativa cDNA clone 14ETL-04-C01, mRNA sequence.

ACCESSION CF278272

VERSION CF278272.1 GI:33655658

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
Unpublished (2003)

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="14ETL-04-C01"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: PCR4-TOPO, Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred.No.1.1e+03; Length 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1470

CF308042 19 bp mRNA linear EST 15-AUG-2003

LOCUS ABR--01-L07.b1 ABR3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABR--01-L07, mRNA sequence.

DEFINITION CF308042

ACCESSION CF308042

VERSION CF308042.1 GI:33679803

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
Unpublished (2003)

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABR--01-L07"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR4-TOPO, Site_1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABR-responsible element binding transcription factor 3 overexpression line."

Query Match

Best Local Similarity 100.0%; Pred.No.1.1e+03; Length 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 4464 TTTT TTTT TTTT TTTT TTTT 4478

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 1471
 AZ465954
 LOCUS 19 bp DNA 1linear GSS 04-OCT-2000
 DEFINITION 1M0276E1SF Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0276E16 F, genomic survey sequence.
 ACCESSION
 AZ465954
 VERSION
 AZ465954.1 GI:10624079
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0276 row: B column: 16
 Seq primer: CGTTGTAAACGACGCCACGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0276E16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gb]|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4463 CTTTTTTTTTTTTT 4477
 Db 5 CTTTTTTTTTTTTT 19

RESULT 1472
 CF282165
 LOCUS 20 bp mRNA 1linear EST 14-AUG-2003
 DEFINITION 14ETL--09-122.G1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--09-122, mRNA sequence.
 ACCESSION
 CF282165
 VERSION
 CF282165.1 GI:33659552
 KEYWORDS
 EST.
 SOURCE
 Oryza sativa
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriarthroideae; Oryzoae; Oryza.
 1 (bases 1 to 20)
 REFERENCE
 AUTHORS
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 TITLE
 Unpublished (2003)
 JOURNAL
 COMMENT
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ETL--09-122"
 /issue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4470 TTTTTTTTTTTTGG 4484
 Db 1 TTTTTTTTTTTTGG 15

RESULT 1473
 AZ596349
 LOCUS 21 bp DNA 1linear GSS 13-DEC-2000
 DEFINITION 1M0409K03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0409K03 R, genomic survey sequence.
 ACCESSION
 AZ596349
 VERSION
 AZ596349.1 GI:11718539
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0409 row: K column: 03
Seq primer: CACACGGAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0409K03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3616 GGGATGGGCTGGCG 3630
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Db 7 GGGATGGGCTGGCG 21

RESULT 1474
A2375417/c 22 bp DNA linear GSS 02-OCT-2000
LOCUS A2375417
DEFINITION IM0128B13R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0128B13 R, genomic survey sequence.
ACCESSION A2375417
VERSION A2375417.1 GI:10489117
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0128 row: E column: 13
Seq primer: CACACGGAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0128B13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTT 4477
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Db 21 CTTTCTTTTCTTTT 7

RESULT 1475
A2425710 23 bp DNA linear GSS 03-OCT-2000
LOCUS A2425710
DEFINITION IM0205L23R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0205L23 R, genomic survey sequence.
ACCESSION A2425710
VERSION A2425710.1 GI:10549723
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0205 row: L column: 23
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGC1M0205123"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAA 4039
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 Db 1 GAAAAA 23

RESULT 1476
 AZ621676 23 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0455J07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0455J07 F, genomic survey sequence.
 ACCESSION AZ621676
 VERSION AZ621676.1 GI:11743962
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0455 row: J column: 07
 Seq primer: CATTGTAAACGACGGCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGC1M0455J07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 15; DB 1; Length 23;
 Best Local Similarity 78.3%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAAACAAATGT 4042
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 Db 1 AAAAAA 23

RESULT 1477
 AZ817623 23 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0087N09F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG2M0087N09 F, genomic survey sequence.
 ACCESSION AZ817623
 VERSION AZ817623.1 GI:12987531
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddum@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0087 row: N column: 09
 Seq primer: CGTGTGTAACGACGGCCACT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES

source

1. 23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0087N09"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male). Was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
 Best Local Similarity 78.3%; Pred. No. 1.6e+03; Length 23;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4020 AAAAAAGAGAGAAACAAATGT 4042
 1 AAAAAAAAAAAAAAAAAATTT 23

RESULT 1478
 CF297907/c 23 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--01-B05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa cDNA clone 7LEAF--01-B05, mRNA sequence.
 ACCESSION CF297907
 VERSION CF297907.1 GI:33669668
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 1 (bases 1 to 23)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.
 Contact: Nahm B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source
 Email: bhnahm@gsbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. 23
 /organism="Oryza sativa"

/mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--01-B05"
 /issue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match
 Best Local Similarity 78.3%; Pred. No. 1.6e+03; Length 23;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAA 4034
 23 AAAAAAGAGAAAAAAAAAAAAA 1

RESULT 1479
 BX560037 23 bp mRNA linear EST 10-OCT-2003
 LOCUS BX560037
 DEFINITION moritans moritans cDNA clone Tse47e08_p1c, mRNA sequence.
 ACCESSION BX560037
 VERSION BX560037.1 GI:33368052
 KEYWORDS EST.
 SOURCE Glossina moritans moritans
 ORGANISM Glossina moritans moritans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 23)
 Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M.,
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina
 moritans moritans and expression analysis of putative immune
 response genes
 Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK.
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.
 Location/Qualifiers
 1. 23
 /organism="Glossina moritans moritans"
 /mol_type="mRNA"
 /sub_species="moritans"
 /db_xref="taxon:37546"
 /clone="Tse47e08_p1c"
 /issue_type="adult infected gut"
 /clone_lib="Glossina moritans moritans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Query Match
 Best Local Similarity 78.3%; Pred. No. 1.6e+03; Length 23;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 4472 TTTTITTTTGTCTGAGACA 4494

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: C column: 09
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0230C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3622 GCGGTGGGGTGGAGAGAGGT 3644
Db 23 GGGGGGGGGGGGGGGGGGGT 1

RESULT 1485
AZ632757 23 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0487M05R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0487M05 R, genomic survey sequence.
ACCESSION AZ632757
VERSION AZ632757.1 GI:11754947
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Scrinata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiser,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0487 row: M column: 05
Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0487M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4461 GACTTTTTTTTTTTTTTTT 4483
Db 1 GTCTTTTTTCTTTTGT 23

RESULT 1486
TA229C12Q 23 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 229C12, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL480862
VERSION AL480862.1 GI:11846631
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 23)
REFERENCE
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.B., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submision
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
mh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TR927/4 GUTac 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelyaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. 23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TR927"
/db_xref="taxon:5691"
/clone="229c12"

Query Match 0.2%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4455 GGCATGACTTTT TTTT TTTT 4477
DB 1 GCGCGCGCGT TTTT TTTT TTTT 23

RESULT 1487

A2812579

LOCUS A2812579 24 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0079G23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0079A23 F, genomic survey sequence.

ACCESSION A2812579
VERSION A2812579.1 GI:12981965

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0079 Row: A Column: 23
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0079A23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAA 4039
DB 2 GAAAAA AAAAAAAAAAAAAA 24

RESULT 1488

A2438069

LOCUS A2438069 24 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0228A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0228A10 F, genomic survey sequence.

ACCESSION A2438069
VERSION A2438069.1 GI:10562178

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0228 Row: A Column: 10
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0228A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4018 AGAAGAGAGAAACAAAT 4040
Db 1 AAAAAAAAAAAAAAAAAAT 23

RESULT 1489

A2764496

LOCUS 24 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0560H02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0560H02 R, genomic survey sequence.
ACCESSION A2764496

VERSION A2764496.1 GI:12879519

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: H column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

Location/Qualifiers

FEATURES

source

1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560H02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473214[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4021 AAGAGAGAGAAACAAATGTT 4043
Db 1 AAAAAAAAAAAAAAAAAATTT 23

RESULT 1490

A2764513

LOCUS 24 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0560D1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0560D1 R, genomic survey sequence.
ACCESSION A2764513

VERSION A2764513.1 GI:12879553

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: D column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

Location/Qualifiers

FEATURES

source

1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560D11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4021 AAAAGAGAGAAACAAATGTT 4043
Db 1 AAAAAAAAAAAAAAAAAATTTT 23

RESULT 1491

AZ448207 24 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0245E16R Mouse 10kb plasmid UUGCM library Mus musculus genomic
DEFINITION Clone UUGCM0245E16 R, genomic survey sequence.

ACCESSION AZ448207
VERSION AZ448207.1 GI:10600777
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 16
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

SOURCE

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0245E16"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGCM library"
/note="Vector: pMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 24;
Best Local Similarity 78.3%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3271 TTGTGTTAGAGAAATGATAA 3293
Db 1 TTTTAAAAAAAAAAAAAAAAA 23

RESULT 1492

AL048782 25 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZP5660013_r1 566 (synonym: hfk42) Homo sapiens cDNA clone
DEFINITION DKFZP5660013, mRNA sequence.

ACCESSION AL048782
VERSION AL048782.1 GI:4727853
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 25)

AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehler, et al.)
JOURNAL Unpublished (1999)

COMMENT Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source Location/Qualifiers

1. 25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP5660013"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1lb="566 (synonym: hfk42)"
/note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match 0.2%; Score 15; DB 1; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4017 GAGAAAAAGAGGAAACAAA 4039
Db 2 GAGGACAAAAAAAAAAAAAAAAA 24

RESULT 1493

CF301712/c 25 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--06-K21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-K21, mRNA sequence.

ACCESSION CF301712
VERSION CF301712.1 GI:33673473
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

/clone.lib="BP Chicken Brain Library"
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
 unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
 5' TGACCTCGAG 3'; 3' adaptor sequence: 5'
 GCGGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
 Clontech (*6854-1)"

Query Match 0.2; Score 15; DB 1; Length 25;
 Best Local Similarity 78.3%; Pred. No. 1.8e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4018 AGAAAAAGAGAGAAAAAATAAT 4040
 Db 23 AAAAAAAAAAAAAAAAAAAAAAT 1

RESULT 1496
 A2381039 25 bp DNA linear GSS 02-OCT-2000
 LOCUS 1M0137N18F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0137N18 F, genomic survey sequence.
 ACCESSION A2381039
 VERSION A2381039.1 GI:10494739
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0137 row: N column: 18
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source

1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0137N18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone.lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2; Score 15; DB 1; Length 25;
 Best Local Similarity 78.3%; Pred. No. 1.8e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4018 AGAAAAAGAGAGAAAAAATAAT 4040
 Db 3 AAAAAAAAAAAAAAAAAAAAAAT 25

RESULT 1497
 A2386891 25 bp DNA linear GSS 02-OCT-2000
 LOCUS 1M0146A08F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGIM0146A08 F, genomic survey sequence.
 ACCESSION A2386891
 VERSION A2386891.1 GI:10500591
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0146 row: A column: 08
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source

1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0146A08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone.lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4018 AGAAAAAGAGAAACAAAT 4040
Db 2 AAAAAAAAAAAAAAAAAAAT 24

RESULT 1498

LOCUS AU265663/c

DEFINITION AU265663 25 bp mRNA linear EST 10-MAY-2002
AU265663 VS Dictyostelium discoideum cDNA clone VSF713 5', mRNA sequence.

ACCESSION AU265663
VERSION AU265663.1 GI:20524461
KEYWORDS EST.

SOURCE Dictyostelium discoideum

ORGANISM Dictyostelium discoideum

REFERENCE Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.

AUTHORS 1 (bases 1 to 25)

Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,

Takeuchi, I., Kohara, Y. and Tanaka, Y.

Population analysis of cDNAs from unicellular and multicellular

stages of Dictyostelium discoideum

Unpublished (2002)

CONTACT: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

Tel: 81-298-53-4664

Fax: 81-298-53-6614

Email: hideko@biol.tsukuba.ac.jp.

FEATURES

source

1..25
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSF713"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.2%; Score 15; DB 1; Length 25;

Best Local Similarity 78.3%; Pred. No. 1.8e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4018 AGAAAAAGAGAAACAAAT 4040
Db 23 AAAAAAAAAAAAAAAAAAAT 1

RESULT 1499

LOCUS T49097/c

DEFINITION T49097 25 bp mRNA linear EST 06-FEB-1995
yb08h08.s1 StrataGene placenta (#937225) Homo sapiens cDNA clone
IMAGE:70623 3' similar to similar to gb:X62744 CLASS II

HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.

ACCESSION T49097 GI:650957

VERSION T49097.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 25)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chippelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favell, A., Gish, N.,
Hawkins, E., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, J.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Warr, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL MEDLINE PUBMED
97044478
8889549
Other ESTs: yb08h08.r1

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL.

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -21ml3

High quality sequence stop: 1.

FEATURES

source

1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:491520"
/db_xref="taxon:9606"
/clone="IMAGE:70623"
/sex="male"
/lab_host="SOLR cells (Kanamycin resistant)"
/clone_lib="Stratagene placenta (#937225)"
/note="Organ: placenta; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

Query Match 0.2%; Score 15; DB 1; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 3271 TTCTTTAAGAGAAATGAA 3293
Db 25 TTCTTTAAAAAAAAAAAAA 3

RESULT 1500

LOCUS TA12F02Q

DEFINITION TA12F02Q 25 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 12102, reverse sequence.
genomic survey sequence.

ACCESSION AL451366

VERSION AL451366.1 GI:11833388

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 25)

Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

COMMENT Rockville, MD. Genomic DNA isolated from a cloned population of

Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. 27
/organism="Oryza sativa"
/mol_type="mRNA"
/cullivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF-06-B07"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABP)"
/note="Vector: pCR4-TOPO, Site_1: EcoRI, leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 15; DB 1; Length 27;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5407 CATTCAAGAAATTAAGACAGA 5429
DB 23 CATTCAAAAAAAAAAAAAA 1

RESULT 1506
AZ495352/c 27 bp DNA linear GSS 05-OCT-2000
LOCUS
DEFINITION 1M0331E14F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0331E14 F, genomic survey sequence.
ACCESSION
AZ495352
VERSION
AZ495352.1 GI:10670743
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: E column: 14
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0331E14"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 27;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAGAAA 4034
DB 23 AAAAGAGAAAAAGAGAGAAA 1

RESULT 1507
AZ953355/c 27 bp DNA linear GSS 27-APR-2001
LOCUS
DEFINITION 2M0218M01R Mouse 10kb plasmid UGCG2M library Mus musculus genomic
clone UGCG2M0218M01 R, genomic survey sequence.
ACCESSION
AZ953355
VERSION
AZ953355.1 GI:13824582
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0218 row: M column: 01
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0218M01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson

Query Match	0.2%	Score 15;	DB 1;	Length 27;
Best Local Similarity	78.3%	Pred. No. 1.9e+03;		
Matches 18; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

RESULT 1508
AL587605/c

LOCUS	AL587605	28 bp	mRNA	linear	EST 02-MAR-2001
DEFINITION	AL587605 BP Chicken Brain Library				
	K05059F11, mRNA sequence.		Gallus gallus	cdna	clone

ACCESSION	AL587605
VERSION	AL587605.1
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE	1 (bases 1 to 28)
AUTHORS	Murray, F.
TITLE	B ϕ chicken Brain library
JOURNAL	Unpublished (2001)
COMMENT	Contact: Frazer Murray

Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@roslin.ac.uk
GCGGCCGGCTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
(+6854-
seq primer: M3P.

FEATURES	source	location/Qualifiers
1..28		
		/organism="Gallus gallus"
		/mol_type="mRNA"
		/db_xref="taxon:9031"
		/clone="ROS059F11"
		/tissue_type="Brain"
		/dev_stage="Unknown"
		/lab_host="DH10B"
		/clone_lid="BP Chicken Brain library"
		/note="vector: pSPOR1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACTCGAG 3', 3' adaptor sequence: 5' GCGCCGCGCTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match	0.2%;	Score 15;	DB 1;	Length 28;
Best Local Similarity	72.0%;	Pred. No. 2e+03;		
Matches 18;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	4010	CTAAATGAGAAAAAGAGAGAAAA	4034
Db	25	CAAAAAAAAAAAAAAAAAANAAAAA	1

RESULT 1509

LOCUS 29 bp mRNA linear EST 07-MAR-1995
DEFINITION y552f07.r3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:65665 5' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16
PRECURSOR (HUMAN) ;, mRNA sequence.

ACCESSION	T67079
VERSION	T67079.1
KEYWORDS	GI:676519
SOURCE	EST.
	Homo sapiens (human)

ORGANISM

REFERENCE
AUTHORS

Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisks, B., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: es@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGB Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGB Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: T7
 High quality sequence stop: 1.

FEATURES
SOURCE

```

/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:65565"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10 (ampicillin resistant)"
/clone_1ib="Soares fetal liver spleen mRNAs"
/note="Organ: Liver and Spleen; Vector: pRTT3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
5' AACGCGAGCATTAATTAACGATCTTTTCTTTTCTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pRTT3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonrado."

```

Query Match	0.2%	Score 15;	DB 1;	Length 29;
Best Local Similarity	75.0%;	Pred. No. 2e+03;		
Matches 18;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

QY 4016 TGAGAAAAAAGAGACAAAACAAA 4039
| | | | | | | | | |
Db 5 TCATAAAAAAAAAAAAAAAAAA 28

RESULT	1510			
AL048741				
LOCUS	29	bp	mRNA	linear
AL048741				EST 04-SEP-2003

```

DEFINITION DKF25656J063_r1.566 (synonym: hfkdx2) Homo sapiens cDNA clone
ACCESSION AL048741 mRNA sequence.
VERSION AL048741.1 GI:4727812
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
    source
        1..29
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKF25656J063"
            /issue_type="Kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_1fb="566 (synonym: hfkdx2)"
            /note="Vector: pAMP1; Site_1: NciI; Site_2: SalI"

Query Match
Best Local Similarity 78.3%; Score 15; DB 1; Length 29;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
    ||||| ||||| ||||| |||||
    7 GGGAAAAAAGAAAAAAGAAAAA 29

RESULT 1511
LOCUS AU267990 29 bp mRNA linear EST 10-MAY-2002
DEFINITION AU267990 VS Dictyostelium discoideum cDNA clone VSH801 5', mRNA
sequence.
ACCESSION AU267990
VERSION AU267990.1 GI:20526788
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
1 (bases 1 to 29)
REFERENCE 1 Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hidekobio1.tsukuba.ac.jp.
FEATURES
    source
        1..29
            /organism="Dictyostelium discoideum"
            /mol_type="mRNA"
            /strain="AX4"
            /db_xref="taxon:44689"
            /clone="VSH801"
            /sex="mat A"
            /dev_stage="vegetative"
            /clone_1fb="VS"

Query Match
0.2%; Score 15; DB 1; Length 29;

```

```

Best Local Similarity 78.3%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4011 TAAATGAGAAAAAGAGAAAA 4033
    ||||| ||||| ||||| |||||
    28 TAAAAAAGAAAAAAGAAAAA 6

RESULT 1512
LOCUS TA244G08P 31 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 244G08, forward sequence.
genomic survey sequence.
ACCESSION AL483539
VERSION AL483539.1 GI:11849040
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 31)
REFERENCE 1 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1..31
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="244G08"

Query Match
0.2%; Score 15; DB 1; Length 31;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
    ||||| ||||| ||||| |||||
    28 GGGAAAAAAGAAAAAAGAAAAA 6

RESULT 1513
LOCUS AL588429 32 bp mRNA linear EST 02-MAR-2001
DEFINITION AL588429 BP Chicken Brain Library Gallus gallus cDNA clone
AL588429
ACCESSION AL588429
VERSION AL588429.1 GI:13193463
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 32)
REFERENCE 1 Murray,F.
AUTHORS

```

TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCAGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
(*6854-)

FEATURES
Source Location/Qualifiers
1..32
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS072C03"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="MDH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TCGACTCGAG 3' ; 3' adaptor sequence: 5'
GCGCCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
Clontech (*6854-1)"

Query Match 0.2%; Score 15; DB 1; Length 32;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 4018 AGAAAAAGAGAAACAAAT 4040
Db 31 AAAAAAAAAAAAAAAAAAAT 9

RESULT 1514
AZ869514 32 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0181107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC2M0181107 R, genomic survey sequence.
ACCESSION AZ869514
VERSION AZ869514.1 GI:13073902
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 32)
Dunn, P., Acovagi, A., Barber, M., Beacorn, T., Duval, B., Hamll, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0181 row: 1 column: 07
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0181107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G14732114|bp|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 15; DB 1; Length 32;
Best Local Similarity 67.7%; Pred. No. 2.1e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Cy 4008 GTCTAAATGAGAAAAAGAGAAACANA 4038
Db 1 GTCTCAAAAACCAAAAAAAAAAAAAA 31

RESULT 1515
BX555533/c 32 bp mRNA linear EST 10-OCT-2003
LOCUS BX555533 Glosina morsitans morsitans adult infected gut Glosina
DEFINITION morsitans morsitans cDNA clone Tse21c01_p1c, mRNA sequence.
ACCESSION BX555533
VERSION BX555533.1 GI:33379519
KEYWORDS EST.
SOURCE Glosina morsitans morsitans
ORGANISM Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossiniidae; Glossina.
REFERENCE
1 (bases 1 to 32)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glosina
morsitans morsitans and expression analysis of putative immune
response genes
TITLE Genome Biol. 4 (10), R63 (2003)
JOURNAL
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
Location/Qualifiers
1..32
/organism="Glosina morsitans morsitans"

FEATURES
Source Location/Qualifiers
1..32
/organism="Mus musculus"

FEATURES
Source Location/Qualifiers
1..32
/organism="Glosina morsitans morsitans"

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/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tseef01_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 15; DB 1; Length 32;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
|||||
32 GAGCAAAAAAAAAAAAAAAAAAAAA 10

RESULT 1516
BX564081/c 33 bp mRNA linear EST 10-OCT-2003
LOCUS BX564081 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tseef01_plc, mRNA sequence.
ACCESSION BX564081
VERSION BX564081.1 GI:33431278
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 33)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Journal Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gtc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source 1..33
location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tseef01_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 15; DB 1; Length 33;
Best Local Similarity 78.3%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAAAAACAAA 4039
|||||
33 GACAAAAAAGAGAAAAACAAA 11

DB 33 GACAAAAAAGAGAAAAACAAA 11

```

```

RESULT 1517
AM246505 18 bp mRNA linear EST 07-JAN-2000
LOCUS AM246505 2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
mRNA sequence.
DEFINITION AM246505
ACCESSION AM246505.1 GI:6589498
VERSION AM246505.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 18)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821585.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/btrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu low Quality Sequence: 18
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: Trace file contained 18 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LCM7 row: D column: 2
High quality sequence stop: 18.
location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821585"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTCTTTT 4481
|||||
1 TTTTTCCTTTTCTTTT 18

RESULT 1518
CF329020 18 bp mRNA linear EST 18-AUG-2003
LOCUS CF329020
DEFINITION NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-D03, mRNA sequence.

```

ACCESSION	CF329020
VERSION	CF329020.1
KEYWORDS	GI:33806277
SOURCE	EST.
ORGANISM	Oryza sativa
TITLE	Oryza sativa
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 18) Kim,Y.S., Jun,K.M., Cheong,P.J., Kim,M.-J., Lee,T.H., Shin,Y.C., Sang,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
JOURNAL	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myoungji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES	Location/Qualifiers
Source	1..18 /organism="Oryza sativa" /mol_type="mRNA" /culivar="Nackdong" /db_xref="taxon:4530" /clone="NAL-04-D03" /tissue_type="callus" /dev_stage="proliferated callus on 2n6 media for 30 days" /lab_host="E.coli DH10B" /clone_lib="Rice callus plasmid cDNA library (NALC)" /note="Vector: pCR4-TOPo; Site 1: EcoRI; mRNA was capped with oligobionucleotides and then used as templates for RT-PCR."
Query Match	0.2% Score 14.8; DB 1; Length 18;
Best Local Similarity	88.9%; Pred.No.1.1e+03;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	4469 TTTTTCCTTTTTTTGTC 4486 1 TTTTTCCTTTTTTACTC 18
Db	
RESULT 1519	
LOCUS	A1371092 19 bp mRNA linear EST 16-PB8-1999
DEFINITION	tat07g09.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2043424 3'
KEYWORDS	similar to TR:Q26195 Q26195 PAI GENE; contains l1.b3 l1
ACCESSION	repetitive element ; , mRNA sequence.
VERSION	A1371092
KEYWORDS	A1371092.1 GI:4149845
SOURCE	EST.
ORGANISM	Homo sapiens (human)
TITLE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 19) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGA), Tumor Gene Index Unpublished (1998)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
COMMENT	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonafdo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E.B. Consortium/LNLW at:

```

www.bio.lim.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 536      Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers

1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2043424"
/issue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_1lb="NCT_CGAP_Brn23"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCATCTGATGAGGAGGCGCGCATCTTTTCTTTTCTTTTCTTTTCTTTT
T 3'], double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and Eco RI
sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

Query Match      0.2%; Score 14.8; DB_1; Length 19;
Beet Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5709 TTTTCTCTCTCTCTCTT 5726
1 TTTTCTCTCTCTCTCTT 18

RESULT 1520
CE309858/c
LOCUS
DEFINITION
ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA
11braty (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.
ACCESSION
CE309858
VERSION
CE309858.1 GI:33681619
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
REFERENCE
1 (bases 1 to 19)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphoridaceae; Oryzaceae; Oryza.
CONTACT: Nahm B.H.
UNPUBLISHED (2003)
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
SOURCE
1. 19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-D16"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI, Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and

```


then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4464 TTTTCTTTCTTTCTTTCTTT 4481
19 TATGTTTCTTTCTTTCTTT 2

RESULT 1521
CF337608/c 19 bp mRNA linear EST 18-AUG-2003

DEFINITION CF337608 JMT--08-C02.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--08-C02, mRNA sequence.

ACCESSION CF337608
VERSION CF337608.1 GI:33823602

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 19)
Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers

1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--08-C02"
/cissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5709 TTTTCTTTCTTTCTTTCTTT 5726
19 TTTTCTTTCTTTCTTTCTTT 2

RESULT 1522

LOCUS A2789309 19 bp DNA linear GSS 16-FEB-2001

DEFINITION 2M0036122R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION A2789309
VERSION A2789309.1 GI:12929974

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0036 Row: L Column: 22

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0036122"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

4463 CTTTCTTTCTTTCTTTCTTT 4480
2 CTTTCTTTCTTTCTTTCTTT 19

RESULT 1523

LOCUS AU007655 20 bp mRNA linear EST 31-JUL-1998

DEFINITION AU007655 Schizosaccharomyces pombe late log phase cDNA

ACCESSION AU007655
VERSION AU007655.1 GI:3344113

KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe

REFERENCE
AUTHORS
TITLE
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
1 (bases 1 to 20)

REFERENCE
AUTHORS
TITLE
Moriyomo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
pombe

JOURNAL
COMMENT
Unpublished (1998)
Contact: Mitsuoki Moriyomo

Genome Research Group
National Institute of Radiological Sciences
9-1, Inage-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: moriyomo@nirs.go.jp.
Location/Qualifiers

FEATURES
source

1.20
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc02339"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, <http://www.nirs.go.jp>)"

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 7113 ATGAATTAATCTTCTCTG 7131
Db 1 ATNAATTCCTTCTCTG 19

RESULT 1524

LOCUS

AZ203903 20 bp DNA linear GSS 29-SEP-2000
DEFINITION IM003B18R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0003B18 R, genomic survey sequence.

ACCESSION AZ203903

VERSION AZ203903.1 GI:10339339

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL COMMENT Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0003 row: B column: 18

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1.20

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UGCGIM0003B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 5723 CTTTGCTGCTTCTCTT 5740
Db 1 CTGTTCTGCTTCTT 18

RESULT 1525

LOCUS

AZ426873 20 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0208L05R Mouse 10kb plasmid UGCGIM library Mus musculus genomic

clone UGCGIM0208L05 R, genomic survey sequence.

ACCESSION AZ426873

VERSION AZ426873.1 GI:10550886

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL COMMENT Contact: Robert B. Weis

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0208 row: L column: 05

Seq primer: CACACGAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1.20

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0208L05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACCTTTTCTTTTCTTTT 4479
DB 18 ACATCTTTTCTTTTCTTTT 1

RESULT 1526
LOCUS AZ772040 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M057461R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
ACCESSION AZ772040
VERSION AZ772040.1 GI:12894936
KEYWORDS GSS,
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: G column: 11
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"

FEATURES
source

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0574G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4477 TTTTTCCTTCTTCTTCTT 4494
DB 2 TTTTTCCTTCTTCTTCTT 19

RESULT 1527
LOCUS AZ943793 20 bp DNA linear GSS 26-APR-2001
DEFINITION 2M020407R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
ACCESSION AZ943793
VERSION AZ943793.1 GI:13808082
KEYWORDS GSS,
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0204 row: A column: 07
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
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/mol_type="genomic DNA"
/strain="C57BL/6J"

FEATURES
source

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/db_xref="taxon:10090"
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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5435 AGCTTTGGCATGACAA 5452
Db 20 AGCTTTGGGTATGATATA 3
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|||||

RESULT 1528
AZ428877 21 bp DNA linear GSS 03-OCT-2000
LOCUS 1M021N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M021N07 R, genomic survey sequence.
ACCESSION AZ428877
VERSION AZ428877.1 GI:10552986
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: N column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
location/Qualifiers
1. 21
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/strain="C57BL/6J"
/db_xref="taxon:10090"

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/sex="Male"  
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6050 TTCTCTCATTCCTTTT 6067
Db 4 TTCTCTCTTCCTTTT 21
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|||||

RESULT 1529
AZ451384 21 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0250D13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0250D13 R, genomic survey sequence.
ACCESSION AZ451384
VERSION AZ451384.1 GI:10607133
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 21.
location/Qualifiers
1. 21
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0250D13"

/sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42n, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3627 GGGGGTGGGAGAGAGCT 3644
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 Db 2 GGGGGTGGGATAGGGGCT 19

RESULT 1530
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 LOCUS AZ512534 21 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0358B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0358B07 F, genomic survey sequence.
 ACCESSION AZ512534
 VERSION AZ512534.1 GI:10693850
 KEYWORDS GSS.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0358 row: B column: 07
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 High quality sequence stop: 21.
 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="UUGC1M0358B07"
 /sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42n, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGGAGAG 3639
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 Db 18 GGGGGGGGGGTGGGAGTG 1

RESULT 1531
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 DEFINITION 2M0281N16R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0281N16 R, genomic survey sequence.
 ACCESSION AZ95847
 VERSION AZ95847.1 GI:13867074
 KEYWORDS GSS.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0281 row: N column: 16
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
 1..21
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC2M0281N16"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

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/clone_11b="Mouse 10Kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g114732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      3617  GGAATGGGCTGGGCTGG 3634
          |||||
          4  GGTAGGGGCTGGGCTGG 21

RESULT 1533
LOCUS      A1707945      22 bp      mRNA      linear      EST 04-JUN-1999
DEFINITION  a634g10.x1 Barstead aorta HPRB6 Homo sapiens cDNA clone
IMAGE:2319138 3 similar to TR:Q62106 Q62106 PROLINE-RICH SALIVARY
PROTEIN; contains element MSRI repetitive element ;, mRNA sequence.
A1707945
ACCESSION  A1707945.1 GI:4997721
VERSION    EST.
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
Hillier,L., Allent,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kizman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Manra,M.,
Martin,J., Moore,B., Scheinberg,K., Steptoe,M., Tan,F.,
Teisling,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: -40UP from Gldco
High quality sequence stop: 1.
location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2319138"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/clone_11b="Barstead aorta HPRB6"
/note="Organ: aorta; Vector: p7T3D-Pac (Pharmacia) with a

```

```

modified polylinker; site 1: EcoRI; site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCAGAACTCAGAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTGGATCGAAC 3' and 5' GTTGGATCG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified p7T3 vector. Library constructed by Bob
Barstead."

Query Match      0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2996  GTCCCCCACCCTCACC 3013
          |||||
          5  GCCCCCCACCCCCACC 22

RESULT 1533
LOCUS      A1738599      22 bp      mRNA      linear      EST 21-DEC-1999
DEFINITION  w139902.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2392658 3'
similar to SW:MNT_HUMAN Q99583 MAX BINDING PROTEIN MNT ;contains
MER22.t1 MSRI repetitive element ;, mRNA sequence.
A1738599
ACCESSION  A1738599.1 GI:5100580
VERSION    EST.
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 383 Std Error: 0.00
Seq primer: -40UP from Gldco
High quality sequence stop: 1.
location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2392658"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_11b="NCI-CGAP-Col6"
/note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

```

OY 2998 CCCCCACCCCTCACCCCA 3015
 Db 4 CCCCACCCCTCACCCCA 21

RESULT 1534

AZ307559 22 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ307559
 DEFINITION 1M0009020F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0009020 F, genomic survey sequence.
 ACCESSION AZ307559
 VERSION AZ307559.1 GI:10346680
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0009 row: O column: 20
 Seq primer: CGTGTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

Location/Qualifiers

1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0009020"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4460 GGAGTTTTTTTTTTTTTT 4477
 Db 2 GGAGTTTTTTTTTTTTTT 19

RESULT 1535

AZ345528 22 bp DNA linear GSS 29-SEP-2000
 LOCUS AZ345528
 DEFINITION 1M0080N03F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGIM0080N03 F, genomic survey sequence.
 ACCESSION AZ345528
 VERSION AZ345528.1 GI:10424765
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0080 row: N column: 03
 Seq primer: CGTGTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

Location/Qualifiers

1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0080N03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 22;
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6682 TTATTTTATTTATATAT 6699


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Db          5  TTATTTTATTATTCAT 22
|||||
RESULT 1536
TA214D07P   22 bp   DNA   linear   GSS 13-DEC-2000
LOCUS      T. brucei sheared genomic DNA clone 214d07, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION  AL479490
VERSION     AL479490.1  GI:11845241
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE     Direct Submission
JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT   Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
            Location/Qualifiers
                1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="214d07"

Query Match          0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred.No.1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy          4460 GGACTTTTTTTTTTTT 4477
|||
Db          5 GGGGTTTTTTTTTTTTT 22

RESULT 1537
TA282D06P/c 22 bp   DNA   linear   GSS 13-DEC-2000
LOCUS      T. brucei sheared genomic DNA clone 282d06, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION  AL487877
VERSION     AL487877.1  GI:11852548
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE  1 (bases 1 to 22)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE     Direct Submission
JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT   Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
            Location/Qualifiers
                1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="214d07"

Query Match          0.2%; Score 14.8; DB 1; Length 22;
Best Local Similarity 88.9%; Pred.No.1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy          4460 GGACTTTTTTTTTTTT 4477
|||
Db          5 GGGGTTTTTTTTTTTTT 22

```

```

COMMENT   Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
            Location/Qualifiers
                1..22
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="282d06"

FEATURES
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2646536"
        /tissue_type="T cell leukemia"
        /cell_line="MGC2"
        /clone_1fb="NIH MGC 2"
        /note="Organ: Blood; Vector: pOTB7a; Library prepared by
            Edge Biosystems."

Query Match          0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred.No.2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 1538
AM327613/c 26 bp   mRNA   linear   EST 28-JAN-2000
LOCUS      dq01b09.y1 NIH_MGC_2 Homo sapiens CDNA clone IMAGE:2646536 3', mRNA
DEFINITION sequence.
ACCESSION  AM327613
VERSION     AM327613.1  GI:6798108
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 26)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Edge Biosystems
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            www-bio.1nl.gov/bdrp/image/image.html
            Plate: LICM0028 row: C column: 17
            Seq primer: M13RPI reverse primer (ABI).
            Location/Qualifiers
                1..26
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                /mol_type="mRNA"
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                /clone="IMAGE:2646536"
                /tissue_type="T cell leukemia"
                /cell_line="MGC2"
                /clone_1fb="NIH MGC 2"
                /note="Organ: Blood; Vector: pOTB7a; Library prepared by
                    Edge Biosystems."

Query Match          0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred.No.2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

Oy	4012	AAATGAGAAAAAGAGAAAACA	4037
Db	26	AAAAAAAAAAAAAAAAAAAAA	1
RESULT 1539			
CF278359/c			
LOCUS			
DEFINITION	14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)		
ACCESSION	Oryza sativa cDNA clone 14ETL--04-D22, mRNA sequence.		
VERSION	CF278359		
KEYWORDS	CF278359.1 GI:33655745		
SOURCE	EST.		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartidae; Oryzaceae; Oryza.		
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.		
TITLE	Large-scale Sequencing Analysis of Rice ESTs		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Bioecon Inc.; Division of Bioscience and Bioinformatics, Myoungil University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr. Location/Qualifiers:		
FEATURES			
source	1..26 /organism="Oryza sativa" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:4530" /clone="14ETL--04-D22" /issue_type="leaf" /lab_stage="14 days after germination" /lab_host="E.coli DH0B" /clone_1fb="Rice etiolated leaf plasmid cDNA library (14ETL)" /note="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."		
Oy	4012	AAATGAGAAAAAGAGAAAACA	4037
Db	26	AAAAAAAAAAAAAAAAAAAAA	1
Query Match			
Best Local Similarity	0.2%; Score 14.8; DB 1; Length 26;		
Matches	19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
RESULT 1540			
CF282426			
LOCUS			
DEFINITION	14ETL--09-P01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)		
ACCESSION	Oryza sativa cDNA clone 14ETL--09-P01, mRNA sequence.		
VERSION	CF282426		
KEYWORDS	CF282426.1 GI:33659813		
SOURCE	EST.		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartidae; Oryzaceae; Oryza.		
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.		
TITLE	Large-scale Sequencing Analysis of Rice ESTs		

JOURNAL COMMENT
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..26
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14BTL-09-P01"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library (14BTL)"
 /note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Basic Local Similarity 73.1%; Pred. No. 2e+03; 7; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches

Oy 4012 AAATGAGAAAAAGAGAGAAACAA 4037
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1541
 CF297087
 LOCUS
 DEFINITION 30DGS--07-L18.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 bativa cDNA clone 30DGS--07-L18, mRNA sequence.
 CF297087
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza bativa
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 26)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea.
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..26
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--07-L18"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: pCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4037
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1542
 CF299701/c

LOCUS 26 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--03-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--03-N03, mRNA sequence.

ACCESSION CF299701
 VERSION CF299701.1 GI:33671462
 KEYWORDS EST.
 SOURCE Oryza sativa

ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatridae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..26
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /culivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--03-N03"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4037
 Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1543
 CF302874/c

LOCUS 26 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF--08-M19, mRNA sequence.

ACCESSION CF302874
 VERSION CF302874.1 GI:33674635
 KEYWORDS EST.
 SOURCE Oryza sativa

ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatridae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 26)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 COMMENT Unpublished (2003)
 CONTACT: Nahm B.H.
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..26
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /culivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--08-M19"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
 Best Local Similarity 73.1%; Pred. No. 2e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAAGAGAAACAA 4037
 Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1544
 CF311369/c

LOCUS 26 bp mRNA linear EST 15-AUG-2003
 DEFINITION ABF--06-J01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa cDNA clone ABF--06-J01, mRNA sequence.

ACCESSION CF311369
 VERSION CF311369.1 GI:33683130
 KEYWORDS EST.
 SOURCE Oryza sativa

ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eriatridae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 26)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

CONTACT: Nahm B.H.
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 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

1..26
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /culivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--06-J01"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1545

LOCUS CF331439 26 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-J02.B1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF331439
VERSION CF331439.1 GI:33811097
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm,B.H.

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Yongin, Kyonggi, Korea
Tel: 82 31 330 6195
Fax: 82 31 321 6355
Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source Location/Qualifiers
1..26

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL-07-002"
/cfeature_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1546

LOCUS AZ359871 26 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0102H23R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0102H23 R, genomic survey sequence.
ACCESSION AZ359871 GI:10473571
VERSION AZ359871.1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Hoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL

CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 23
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source Location/Qualifiers
1..26

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0102H23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g14732114[9b]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAAACAA 4037
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1547

LOCUS AZ376664 26 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0130E08R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0130E08 R, genomic survey sequence.
ACCESSION AZ376664 GI:10490364
VERSION AZ376664.1
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longacre, R., Mahmoud, M., Meenen, E., Pedersen, T.,
 Kelly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
JOURNAL
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 unpublished (2000)
COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddu@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0150 row: D column: 13
 Seq primer: CACACAGAAACAGCATGACG
 Class: plasmid ends
 High quality sequence stop: 26.
FEATURES
 source
 1..26
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0150D13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: pMD42ny. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repeated with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gll4732114[gb]/AF129072.1) a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

RESULT	1552
AZ624441/c	
LOCUS	AZ624441 26 bp DNA linear GSS 13-DEC-2000
DEFINITION	U0463007F Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGM046307 F, genomic sequence.
ACCESSION	AZ624441
VERSION	AZ624441.1 GI:11746631
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isaiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

RESULT	1553
LOCUS	A2627846/c
DEFINITION	A2627846 Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGM0474H08 F, genomic survey sequence.
ACCESSION	A2627846
VERSION	A2627846.1 GI:11750132
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,W., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nedehausen,A. and Wright,D.,Wels,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: H column: 08
Seq primer: CCGTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0474H08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UGGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAA 4037
DB 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1554
AZ80453/c 26 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0525H1SR Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGGCM0525H1S R, genomic survey sequence.
ACCESSION AZ80453
VERSION AZ80453.1 GI:11789108
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: H column: 15
Seq primer: CACACGAAACAGCATGAC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0525H1S"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UGGCM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAACAA 4037
DB 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1555
AZ800453/c 26 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0058023F Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGG2M0058023 F, genomic survey sequence.
ACCESSION AZ800453
VERSION AZ800453.1 GI:12952583
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: 0 column: 23
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

source

1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M058023"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.14; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAGAGAAACAA 4037

Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1556
AZ963974/c 26 bp DNA linear GSS 27-APR-2001
LOCUS 2M023N01F Mouse 10kb plasmid UUC2M library Mus musculus genomic
DEFINITION clone UUC2M023N01 F, genomic survey sequence.
ACCESSION AZ963974
VERSION AZ963974.1 GI:13835201
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Jellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

COMMENT

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University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: N column: 01
Seq primer: CGTTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

source

1. 26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0233N01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.14; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAGAGAAACAA 4037

Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1557
TA324D07P 26 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 324d07, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL493390
VERSION AL493390.1 GI:11867755
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 26)
Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Actin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The $v + i$ method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrel, Oxford University Press, 1999).

Email: nelseyed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..26

/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="324d07"

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03; 7; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAATGAGAAAAAGAGAAAAACAA 4037
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 26

Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1558

AZ355083

LOCUS

1M0094D14R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0094D14 R, genomic survey sequence.

DEFINITION

AZ355083 26 bp DNA linear GSS 02-OCT-2000
clone UGCGIM0094D14 R, genomic survey sequence.

ACCESSION

AZ355083.1 GI:10467134
GSS.

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UGCGIM0094D14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES

source

1..26

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0094D14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.8; DB 1; Length 26;
Best Local Similarity 73.1%; Pred. No. 2e+03; 7; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4013 AAATGAGAAAAAGAGAAAAACAA 4038
|||||
1 AAAAAAAAAAAAAAAAAAAAAA 26

Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1559

AZ623156

LOCUS

1M0460L01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0460L01 R, genomic survey sequence.

DEFINITION

AZ623156 26 bp DNA linear GSS 13-DEC-2000
clone UGCGIM0460L01 R, genomic survey sequence.

ACCESSION

AZ623156.1 GI:11745346
GSS.

VERSION

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 01
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0460L01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

FEATURES

source

1..26

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0460L01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0243 Row: N Column: 14
 Seq primer: CACACAGAAACAGCTATGAC
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

source

1..27
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MUGCM0243N14"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.2%; Score 14.8; DB 1; Length 27;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAA 4037

Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1563
 NS1845/c
 LOCUS 27 bp mRNA linear EST 30-JAN-1997
 DEFINITION Y202d07.g1 Soares multiple sclerosis 2NbhMSP Homo sapiens cDNA
 clone IMAGE:281865.3 similar to gb:W51564 SRRM RESPONSE FACTOR
 ACCESSION NS1845
 VERSION NS1845.1 GI:1193011
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL
 MEDLINE 97044478
 PUBMED 8889349
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estowatson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 450 Std Error: 0.00
 Seq primer: m3 -40 forward
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1..27
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3900397"
 /db_xref="taxon:9606"
 /clone="IMAGE:281869"
 /sex="male"
 /issue_type="multiple sclerosis lesions"
 /dev_stage="Age 46"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_1lb="Soares multiple sclerosis 2NbhMSP"
 /note="Vector: pT73D (Pharmacia) with a modified polylinker V-type phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGCTTCATCGATGAGGAGCGCCGATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)."

Query Match

Best Local Similarity 70.4%; Score 14.8; DB 1; Length 27;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAA 4038

Db 27 AAATTTTAAAAAAAAAAAAAAAA 1

RESULT 1564
 T52836/c
 LOCUS 28 bp mRNA linear EST 06-FEB-1995
 DEFINITION ya81b09.g1 Striatum ovary (H93717) Homo sapiens cDNA clone
 IMAGE:66057.3 similar to gb:X53463 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.
 ACCESSION T52836
 VERSION T52836.1 GI:654696
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL

Genome Res. 6 (9), 807-828 (1996)

PUBMED
COMMENT

8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 51

High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNU. This clone is available royalty-free
through LNU; contact the IMAGE Consortium (info@image.lnu.gov)
for further information. Trace considered overall poor quality
Insert Length: 51 Std Error: 0.00
Seq primer: -21ml3

FEATURES
source

High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:504314"
/db_xref="taxon:9606"
/clone="IMAGE:68057"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'
GAATTCGCGACGAC 3' ~3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'."

Query Match 0.24; Score 14.8; DB 1; Length 28;
Best Local Similarity 73.1%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAA 4037
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1565
A2819924 29 bp DNA linear GSS 20-FEB-2001
LOCUS A2819924
DEFINITION 2M0091A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0091A19 R, genomic survey sequence.
ACCESSION A2819924
VERSION A2819924.1 GI:12989832
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: A column: 19
Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1[473214]gb[4739072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.24; Score 14.8; DB 1; Length 29;
Best Local Similarity 73.1%; Pred. No. 2.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAAGAGAAACAA 4037
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1566
A2492630/c 29 bp DNA linear GSS 05-OCT-2000
LOCUS A2492630/c
DEFINITION 1M0326B2R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0326B2 R, genomic survey sequence.
ACCESSION A2492630
VERSION A2492630.1 GI:1066537
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0326 row: B column: 22
Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"


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SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..29
        /organism="Oryza sativa"
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        /cultivar="Nackdong"
        /db_xref="taxon:4530"
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        /lab_host="E.coli DH10B"
        /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.2%; Score 14.8; DB 1; Length 29;
Best Local Similarity 73.1%; Pred. No.2.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4014 AATGAGAAAAAGAGACAAACAAA 4039
        |||||
        26 AAGCGTAAAAAAGAGAAAAA 1

RESULT 1570
LOCUS      CF295370
DEFINITION 30DGS--05-E14.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--05-E14, mRNA sequence.
ACCESSION  CF295370
VERSION     CF295370.1 GI:33664403
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..29
        /organism="Oryza sativa"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
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        /lab_host="E.coli DH10B"
        /clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
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            RT-PCR."

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/tissue_type="leaf"
/dev_stage="30 days after germination"
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/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.2%; Score 14.8; DB 1; Length 29;
Best Local Similarity 73.1%; Pred. No.2.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4020 AAAAAAGAGAAAAACAAATGTTAT 4045
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        27 AAAAAAAGAAAAAAGCACTGTCAT 2

RESULT 1571
LOCUS      CF293772
DEFINITION 30DGS--03-B05.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
            sativa cDNA clone 30DGS--03-B05, mRNA sequence.
ACCESSION  CF293772
VERSION     CF293772.1 GI:33662805
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Eriactoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc., Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..29
        /organism="Oryza sativa"
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        /cultivar="Nackdong"
        /db_xref="taxon:4530"
        /clone="30DGS--03-B05"
        /tissue_type="leaf"
        /dev_stage="30 days after germination"
        /lab_host="E.coli DH10B"
        /clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
        /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.2%; Score 14.8; DB 1; Length 29;
Best Local Similarity 73.1%; Pred. No.2.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4020 AAAAAAGAGAAAAACAAATGTTAT 4045
        |||||
        27 AAAAAAAGAAAAAAGCACTGTCAT 2

RESULT 1572
LOCUS      CF311684
DEFINITION ABF--07-A15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-A15, mRNA sequence.
ACCESSION  CF311684
VERSION     CF311684.1 GI:33683445

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KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 31)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
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1..31
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.2%; Score 14.8; DB 1; Length 31;
Best Local Similarity 73.1%; Pred. No. 2.2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAGAAACAAATGTTAT 4045
DB 29 AAAAAAAAAAAAAAAAACACTGTCAT 4

RESULT 1573
CFJ12635 31 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--08-H15.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-H15, mRNA sequence.
ACCESSION CFJ12635
VERSION CFJ12635.1 GI:33684396
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 31)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..31
/organism="Oryza sativa"

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 31)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..31
/organism="Oryza sativa"

Query Match 0.2%; Score 14.8; DB 1; Length 33;
Best Local Similarity 73.1%; Pred. No. 2.2e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAGAAACAAATGTTAT 4045
DB 30 AAAAAAAAAAAAAAAAACACTGTCAT 5

RESULT 1574
BX551140/c 33 bp mRNA linear EST 10-OCT-2003
LOCUS BX551140 GLOSSINA MORITANS MORITANS ADULT INFECTED GUT GLOSSINA MORITANS MORITANS CDNA CLONE TSE116G12_PLC, mRNA sequence.
DEFINITION BX551140
ACCESSION BX551140
VERSION BX551140.1 GI:33374994
KEYWORDS EST.
SOURCE GLOSSINA MORITANS MORITANS
ORGANISM Glossina moritans moritans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 33)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, D., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina moritans moritans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22861942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
Location/Qualifiers

FEATURES
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/organism="Glossina moritans moritans"
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/db_xref="taxon:37546"
/clone="Tse116g12 plc"
/issue_type="adult infected gut"
/clone_lib="Glossina moritans moritans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAGAGAAACAA 4037
 Db 33 AAAACAAAAAATACTA 8

RESULT 1575
 BXS66898/c
 LOCUS
 DEFINITION BXS66898 Glossina morsitans morsitans adult infected gut Glossina
 morsitans morsitans cDNA clone Tse84h03_p1c, mRNA sequence.
 ACCESSION BXS66898
 VERSION BXS66898.1 GI:33433863
 KEYWORDS EST.
 SOURCE
 ORGANISM Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 33)
 Lehane, M.J., Aksoy, S., Gibson, W., Kertou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
 response genes
 Genome Biol. 4 (10), R63 (2003)
 14519198
 JOURNAL MEDLINE
 PUBMED
 COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.
 Location/Qualifiers
 1..33
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
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 /clone="Tse84h03_p1c"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Query Match 0.2%; Score 14.8; DB 1; Length 33;
 Best Local Similarity 73.1%; Pred. No. 2.2e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAATGAGAAAAGAGAAACAA 4037
 Db 33 AAAACAAAAAATACTA 8

RESULT 1576
 CF276638/c
 LOCUS
 DEFINITION CF276638 21 bp mRNA linear EST 14-AUG-2003
 14ETL--01-N19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa cDNA clone 14ETL--01-N19, mRNA sequence.
 ACCESSION CF276638
 VERSION CF276638.1 GI:33654024
 KEYWORDS EST.
 SOURCE
 ORGANISM Oryza sativa
 Oryza sativa

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.-K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultiivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ETL--01-N19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 1.6e+03;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4019 GAAAAAGAGAAACAAA 4039
 Db 21 GAAAAAATACTA 1

RESULT 1577
 A2597932/c
 LOCUS
 DEFINITION A2597932 21 bp DNA linear GSS 13-DEC-2000
 IM0412D23F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
 clone UNGC1M0412D23 F, genomic survey sequence.
 A2597932
 A2597932.1 GI:11720122
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0412 row: D column: 23
 Seq primer: CGTTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES
source

Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0412D23"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGA 4032
|||||
21 AAAAAAAAAAAAAAAAAA 1

Db 21 AAAAAAAAAAAAAAAAAA 1

RESULT 1578
CF280925/c 21 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--07-M14.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa cDNA clone 14ETL--07-M14, mRNA sequence.
ACCESSION CF280925
VERSION CF280925.1 GI:33658311
KEYWORDS EST.

SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioeconomy and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

TITLE
JOURNAL
COMMENT

FEATURES
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1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/issue_type="leaf"
/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4031 AAAACAAATGTAATTTTAT 4051
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21 AAAAAAAAAATTTTTTTTTT 1

Db 21 AAAAAAAAAATTTTTTTTTT 1

RESULT 1579
A2339966 21 bp DNA linear GSS 29-SEP-2000
LOCUS 1M007111.R Mouse 10kb plasmid UGC1M library Mus musculus genomic
DEFINITION clone UGC1M007111 R, genomic survey sequence.
ACCESSION A2339966
VERSION A2339966.1 GI:10414760
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Isham,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: 1 column: 11
Seq primer: CACACGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M007111"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGCTGGGGCTGGAGAGAG 3642
DB 21 GGGGGGGGGGGGGGGGGG 1

RESULT 1582

AZ483617 21 bp DNA linear GSS 05-OCT-2000
LOCUS AZ483617/c
DEFINITION 1M0309A05R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0309A05 R, genomic survey sequence.

ACCESSION AZ483617
VERSION AZ483617.1 GI:10647772

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weis
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0309A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4468 TTTTGTGTTTGTGTTT 4488
DB 21 TTTTGTGTTTGTGTTT 1

RESULT 1583

AZ499846 21 bp DNA linear GSS 05-OCT-2000
LOCUS AZ499846/c
DEFINITION 1M0337E23R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0337E23 R, genomic survey sequence.

ACCESSION AZ499846
VERSION AZ499846.1 GI:10679079

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weis
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0337 row: E column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

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/clone="UGCG1M0337E23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3623 GGGTGGGGGTGGAGAGAGAG 3643
|||||
Db 21 GGGGGGGGGGGGGGGGGAGG 1

RESULT 1584
AZ583408/c

LOCUS 21 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0378N23r Mouse 10kb plasmid UGUC1M library Mus musculus genomic
clone UGUC1M0378N23 F, genomic survey sequence.

ACCESSION AZ583408
VERSION AZ583408.1 GI:11703261

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0378 row: N column: 23

Seq primer: GGTGTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGUC1M0378N23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3615 GGGGAATGGGGTGGGGTGGG 3635
|||||
Db 21 GGGGAGAGGGGGGGGGGGGGG 1

RESULT 1585

AZ589098/c

LOCUS 21 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0397B19R Mouse 10kb plasmid UGUC1M library Mus musculus genomic
clone UGUC1M0397B19 R, genomic survey sequence.

ACCESSION AZ589098
VERSION AZ589098.1 GI:11711288

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiser, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0397 row: B column: 19

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGUC1M0397B19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5327 TCTCTTTGCTGCTACTCTCT 5347
Db 21 TCTCTCTCTCTCTCTCTCTCT 1

RESULT 1586

A2627978

LOCUS

DEFINITION A2627978 21 bp DNA linear GSS 13-DEC-2000
1M0476104F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0476104 F, genomic survey sequence.

ACCESSION

A2627978

VERSION

A2627978.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT/
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plates: 0476 row: L column: 04
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1.21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0476104"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.2%; Score 14.6; DB 1; Length 21;

Best Local Similarity 81.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5327 TCTCTTTGCTGCTACTCTCT 5347
Db 1 TCTCTCTCTCTCTCTCTCTCT 21

RESULT 1587

A2770188/c

LOCUS

DEFINITION A2770188 21 bp DNA linear GSS 16-FEB-2001
1M0571A12R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0571A12 R, genomic survey sequence.

ACCESSION

A2770188

VERSION

A2770188.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT/
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plates: 0571 row: A column: 12
Seq primer: CACACAGAAACGCTATGAC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES

source

1.21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0571A12"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.2%; Score 14.6; DB 1; Length 21;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3004 CCCCTACCCCATCTTGTGC 3024

Db 21 CCCCTCCCCCATGTATGTAC 1

RESULT 1588
 AZ961893/c 21 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0230E06R Mouse 10kb plasmid UGCG2M library Mus musculus genomic
 DEFINITION clone UGCG2M0230E06 R, genomic survey sequence.
 ACCESSION AZ961893
 VERSION AZ961893.1 GI:13833120
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0230 row: E column: 06
 Seq primer: CACACAGCAACAGCTATGACG
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0230E06"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG2M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGTGGAGAGAG 3642

Db 21 GGGGGGGGGGGGGGGGGG 1

RESULT 1589
 AZ374487 22 bp DNA linear GSS 02-OCT-2000
 LOCUS 1M0127H16F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 DEFINITION clone UGCG1M0127H16 F, genomic survey sequence.
 ACCESSION AZ374487
 VERSION AZ374487.1 GI:10488187
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0127 row: H column: 16
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0127H16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4019 GAAAAAGAGAAAAA 4039
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 Db 1 GAAAAAGAGAAAAA 21

RESULT 1590
 A1439277 22 bp mRNA linear EST 09-MAR-1999
 LOCUS t154602.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134250 3'
 DEFINITION similar to TR:Q17089 Q17089 COLLAGEN; contains element MER22
 repetitive element; mRNA sequence.

ACCESSION A1439277
 VERSION A1439277
 KEYWORDS GI:4303196
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 22)
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLMT at:
 www.bio.lnl.gov/bbr/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1..22
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2134250"
 /tissue_type="lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Lym12"
 /note="Organ: lymph node; Vector: pCMV-SPORT6, Site 1:
 SalI; Site 2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3390 CCAGCTGCACCCCACTT 3410
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 Db 1 CCCGCCCACTT 21

RESULT 1591
 A1439277 22 bp mRNA linear EST 25-APR-2002
 LOCUS A1439277
 DEFINITION A1439277 3'-directed mouse cDNA library Mus musculus cDNA clone
 BED0016802 3', mRNA sequence.
 ACCESSION A1439277
 VERSION A1439277
 KEYWORDS GI:20327801
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Kato, K. and Matoba, R.
 Generation of expressed sequence tags from mouse brain

JOURNAL Unpublished (2002)
 COMMENT Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkatob@isct-nara.ac.jp
 URL: http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES
 source
 1..22
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 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="BED0016802"
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 /clone_lib="3'-directed mouse cDNA library"

Query Match 0.2%; Score 14.6; DB 1; Length 22;
 Best Local Similarity 81.0%; Pred. No. 1.7e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1531 TTCTCATGATGATGATC 1551
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 Db 21 TTCTCATGATGATGATC 1

RESULT 1592
 A2447246 22 bp DNA linear GSS 04-OCT-2000
 LOCUS A2447246
 DEFINITION 1M0244E23F Mouse 10kb plasmid UUGCM library Mus musculus genomic
 clone UUGCM0244E23 F, genomic survey sequence.

ACCESSION A2447246
 VERSION A2447246
 KEYWORDS GI:10599040
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D. Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0244 row: E column: 23
 Seq primer: CGTGTGAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCM0244E23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cy 3623 GGGTGGGGGTGGAGAGAGG 3643
Db 22 GGGGGGGGGGGGGGGGGGG 2

RESULT 1593

AZ464354 22 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION IM0273M1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0273M1 R, genomic survey sequence.

ACCESSION AZ464354
VERSION
KEYWORDS AZ464354.1 GI:10622479
GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0273 row: M column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0273M1"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cy 5326 TTCTCTCTTGGCTCACTCTC 5346
Db 2 TTCTCTCTCTCTCTCTCTC 2

RESULT 1594

AZ611419/c 22 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION IM0437D1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0437D1 R, genomic survey sequence.

ACCESSION AZ611419
VERSION
KEYWORDS AZ611419.1 GI:11733609
GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0437 row: D column: 15

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0437D1"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.24; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3623 GGGTGGGGGTGGGAGAGAGAG 3643
Db 22 GGGGGGGGGGGGGGGGGGGAGG 2

RESULT 1595
LOCUS A2766712 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0564A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0564A03 R, genomic survey sequence.

ACCESSION A2766712
VERSION A2766712.1 GI:12884063
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: 0 column: 03
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source Location/Qualifiers
1..22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564A03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

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Query Match 0.24; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3622 GGGTGGGGGTGGGAGAGAGAG 3642
Db 21 GGGGTGGGGGGGGGGGGGGGGG 1

RESULT 1596
LOCUS A2769521 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0570018F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0570018 F, genomic survey sequence.

ACCESSION A2769521
VERSION A2769521.1 GI:12889741
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.

AUTHORS Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: 0 column: 18
Seq primer: CGTTGTAAGACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source Location/Qualifiers
1..22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0570018"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adopted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g114732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adopted mouse DNA was annealed to adopted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3623 GGGTGGGGGTGGAGAGAGG 3643
DB 22 GGGGGGGGGTGGGGGGGGG 2

RESULT 1597
A2776605/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0010119F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCG2M0010119 F, genomic survey sequence.

ACCESSION A2776605
VERSION A2776605.1 GI:12904372
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: 1 column: 19
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0010119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

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Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 55 GGCACGAGGCTGCGGGGC 75
DB 22 GGGACGACGAGCTGAGGAGC 2

RESULT 1598
A2778745 22 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0014M08F Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCG2M0014M08 F, genomic survey sequence.

ACCESSION A2778745
VERSION A2778745.1 GI:12908699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: M column: 08
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 22.

FEATURES

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/strain="C57BL/6J"
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/clone="UGCG2M0014M08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

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Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5885 CCTTACTGCAAGAACCAAG 5905
DB 1 CCTTGACTACAGAAATCAAG 21

RESULT 1599

LOCUS AZ868780 22 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0180E12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ868780
VERSION AZ868780.1 GI:13072436
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (baes 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: E column: 12
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180E12"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3615 GGGGAATGGGCTGGGGCTGGG 3635
DB 2 GGGGTTGGGGGTGAGGGTGGG 22

RESULT 1600

LOCUS AZ958390 22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0225J07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION AZ958390
VERSION AZ958390.1 GI:13829617
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (baes 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: J column: 07
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1. 22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0225J07"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3615 GCGGATGCGGTGGGGTGGG 3635
Db 21 GGGGATTTGGGGGGGGGGG 1

RESULT 1601
AZ974046/c
LOCUS 22 bp DNA linear GSS 27-APR-2001
DEFINITION 2M024GC01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M024GC01 R, genomic survey sequence.
ACCESSION AZ974046
VERSION AZ974046
KEYWORDS GI:13845273
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellin, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: C column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
SOURCE
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M024GC01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3622 GGGGTGGCGTGGAGAGAGAG 3642
Db 21 GGGGGGGGGGGGGGGGGGAG 1

RESULT 1602
TA8C02P
LOCUS 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 8c02, forward sequence, genomic survey sequence.
ACCESSION AL452598
VERSION AL452598.1 GI:11861142
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers

FEATURES
SOURCE
1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="8c02"

Query Match 0.2%; Score 14.6; DB 1; Length 22;
Best Local Similarity 81.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3652 TCCCTTCTCCTTATCTCTCC 3872
Db 2 TCCCTTGGCGATATCTCTCC 22

RESULT 1603
AZ380872
LOCUS 23 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0137H02P Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0137H02 F, genomic survey sequence.
ACCESSION AZ380872

VERSION AZ380872.1 GI:10494572
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL Plasmid inserts
 COMMENT Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY of Utah Genome Center
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0137 row: H column: 02
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
 1. 23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0137H02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 23;
 Best Local Similarity 81.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4031 AAAACAAATGTTATTTTAT 4051
 DB 22 AAAAAAAAAATTTTATTTT 2

RESULT 1604
 AZ514388/c 24 bp DNA linear GSS 05-OCT-2000
 LOCUS AZ514388
 DEFINITION IM0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0361H04 F, genomic survey sequence.
 ACCESSION AZ514388
 VERSION AZ514388.1 GI:10695704

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL Plasmid inserts
 COMMENT Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY of Utah Genome Center
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0361 row: H column: 04
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1. 24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0361H04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.6; DB 1; Length 24;
 Best Local Similarity 81.0%; Pred. No. 1.9e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4013 AATGAGAAAAAGAGAAA 4033
 DB 24 AAAAAAAAAAAAAAGAGAAA 4

RESULT 1605
 AZ485624 26 bp DNA linear GSS 05-OCT-2000
 LOCUS AZ485624
 DEFINITION IM0313H1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0313H1 F, genomic survey sequence.
 ACCESSION AZ485624
 VERSION AZ485624.1 GI:10651606

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 26)
AUTHORS	Dunn, P., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Niedermaier, A. and Wright, D., Weis, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weis University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0313 row: H column: 11 Seq primer: GGTGTAAACGACGCGCCAGT Class: plasmid ends High quality sequence stop: 26. Location/Qualifiers 1..26 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="U08C1M0313H11" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid U08C1M library" /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	0.2%; Score 14.6; DB 1; Length 26;
Best Local Similarity	81.0%; Pred. 2.1e-03;
Matches	17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
CY	4020 AAAAAAGAGCAAAACAAAT 4040
DB	1 AAAAAAAAAAAAAAAAAAAT 21
RESULT 1606	
CF639306	
LOCUS	CF639306 26 bp mRNA linear EST 02-OCT-2003
DEFINITION	D14 A02 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
ACCESSION	CF639306
VERSION	CF639306.1 GI:37403783
KEYWORDS	EST.
SOURCE	Ustilago maydis

ORGANISM Uterlago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

REFERENCE 1 (bases 1 to 26)
AUTHORS Nugent,K.G., Choffe,K. and Saville,B.J.
TITLE Gene Expression during Uterlago maydis Diploid Filamentous Growth:
Esi Library Creation and Analyses
JOURNAL Unpublished (2003)
COMMENT Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-DM-D126/7-014-UTM row: 02 column: A
Seq primer: T7 Reverse (5' GAGTATACGACTCACTAATGAGG 3')
High quality sequence stop: 26.
Location/Qualifiers
1..26
/organism="Uterlago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="mycelia"
/dev_stage="Filamentous diploid"
/clone_id="Filamentous Forced Diploid"
/note="Vector: pSPORT; mRNA was extracted and
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."

Query Match 0.23; Score 14.6; DB 1; Length 26;
Best Local Similarity 77.3%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4018 AGAAAAAGAGAGAAAAA 4039
Db 4 AAAAAAAAAAAAAAAAAAAAA 25

RESULT 1607
T52979/c
LOCUS T52979 27 bp mRNA linear EST 06-FEB-1995
DEFINITION ya28e08.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone
IMAGE:68198 3' similar to (similar to gb:D00174 ALPHA-2-ANTIPLASMIN
PRECUSOR (HUMAN), mRNA sequence.
T52979
ACCESSION T52979.1 GI:654839
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Euthetia; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 27)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Roiliff,T., Schellberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
8889549
Other ESTs: ya28e08.r1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu


```

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="GDB:3881200"
/db_xref="taxon:9606"
/clone="IMAGE:271558"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Scares melanocyte 2NBHm"
/notes="vector: pRTTID (pharmacia) with a modified
polylinker site_1: Not I, site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5,
TGTTACCATCTGGAAGTGGAGCGCGCCAGTCTTTTCTTTTCTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTTID vector
(pharmacia). library constructed by Benito Soares and
M.Felicia Bonaldo. RNA from normal foreskin melanocytes
(F5374) was kindly provided by Dr. Anthony P. Albino."

Query Match
Best Local Similarity 73.9%; Pred.No.2.2e+03;
Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0,

0.2%; Score 14.6; DB 1; Length 30;

OY 4012 AAATGAGAAAAAGAGAGAAAA 4034
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
|||||
|||||
|||||
|||||

RESULT 1611
CF317778
LOCUS CF317778 16 bp mRNA EST 15-AUG-2003
DEFINITION HD--07-J13.b1 OshDACL-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.
CF317778
ACCESSION CF317778.1 GI:33689539
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.D., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,U.K., Kim,Y.-K. and Nahm,B.H.

```

TITLE	Large-scale Sequencing Analysis of Rice ESTs									
JOURNAL	Unpublished (2003)									
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr. Location/Qualifiers									
FEATURES	source									
	1. .16 /organism="Oryza sativa" /mol_type="mRNA" /culivar="Nackdong" /db_xref="taxon:4530" /clone="HD-07-U13" /tissue_type="callus" /dev_stage="proliferated callus on 2N6 media for 2 weeks" /lab_host="E.coli DH10B" /clone_1lb="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)" /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."									
Query Match	0.2%; Score 14.4; DB 1; Length 16;									
Best Local Similarity	93.8%; Pred. No. 1e+03;									
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Oy	4464 TTTT TTTT TTTT TTTT TTTT 4479 1 TTGTGTTTTTTTTTTT 16									
Db	1 TTGTGTTTTTTTTTTT 16									
RESULT 1612										
LOCUS	AM247165 17 bp mRNA linear EST 07-JAN-2000									
DEFINITION	2819675.spprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819675 3', mRNA sequence.									
ACCESSION	AM247165									
VERSION	AM247165.1 GI:5590158									
KEYWORDS	EST.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
REFERENCE	1 (bases 1 to 17) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)									
AUTHORS	Other ESTs: 2819675.spprime									
TITLE	Contact: Robert Strausberg, Ph.D.									
JOURNAL	Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNt) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNt at: www-bio.lnl.gov/bdrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 17 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Plate: L1CM2 row: D column: 12 High quality sequence stop: 17.									
COMMENT	Location/Qualifiers									
FEATURES	1. .17									
SOURCE										

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819675"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB; Site: 1; XhoI; Site: 2;
ECORI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.2%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4479
 DB 2 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1613
 CFJ18426/c 19 bp mRNA linear EST 15-AUG-2003
 LOCUS HD-08-120.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 ACCESSION CFJ18426
 VERSION CFJ18426.1 GI:335690187
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 19)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES
 source 1..19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-08-120"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /notes="Vector: PCR4-TOPO; Site: 1; EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 5027 AGGAGCAGCTCAGTG 5042
DB 19,AGGAGCAGCTCATTG 4

RESULT 1614
LOCUS AZ656129 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0531C04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0531C04 R, genomic survey sequence.
ACCESSION AZ656129
VERSION AZ656129.1 GI:11793275
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0531 row: C column: 04
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence scop: 19.
Location/Qualifiers
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FEATURES
 source 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0531C04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114[gblAF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2042 CAGCAGTGTAAGCAG 2057

Query Match	0.28;	Score 14.4;	DB 1;	Length 20;
Best Local Similarity	93.8%;	Pred. NO. 1.55+00;		
Matches 15;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	4464	TTTTTTTTTTTTTTTT	4479	
Db	20	TTTTTTTTTTTTTTTT	5	

Query Match	0.2%	Score 14.4	DB 1	length 22
Best Local Similarity	93.8%	Pred. No. 1.8e+03		
Matches 15; Conservative	0	Mismatches 1	Indels 0	Gaps 0
QY	2866	GCAAGAGAGAGGAGG	2881	
b	16	GGAGAGAGAGGAGG	1	

```

RESULT 1619
A2764528/c 22 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION IM0560L14R Mouse 10kb plasmid U0CGIM library Mus musculus genomic
clone U0CGIM0560L14 R, genomic survey sequence.
ACCESSION
A2764528
VERSION
A2764528.1 GI:12879583
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 14
Seq primer: CACACAGCAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES
location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U0CGIM0560L14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U0CGIM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4462 ACTTTTCTTTTCTTTT 4477
| | | | | | | | | | | | | | | | | | | | |
Db 16 AATTTTCTTTTCTTTT 1

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```

TA193A07P/c
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 193A07, forward sequence,
genomic survey sequence.
ACCESSION
AL478342
VERSION
AL478342.1 GI:11842152
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 22)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
FEATURES
location/Qualifiers
1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="193A07"
Query Match 0.2%; Score 14.4; DB 1; Length 22;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4462 ACTTTTCTTTTCTTTT 4477
| | | | | | | | | | | | | | | | | | | | |
Db 16 AATTTTCTTTTCTTTT 1

```

```

RESULT 1621
A2764519 24 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION IM0560P14R Mouse 10kb plasmid U0CGIM library Mus musculus genomic
clone U0CGIM0560P14 R, genomic survey sequence.
ACCESSION
A2764519
VERSION
A2764519.1 GI:12879566
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

```

```

RESULT 1620
A2764519 24 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION IM0560P14R Mouse 10kb plasmid U0CGIM library Mus musculus genomic
clone U0CGIM0560P14 R, genomic survey sequence.
ACCESSION
A2764519
VERSION
A2764519.1 GI:12879566
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

```

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: P column: 11
Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source

1. .24
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0560P11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4022 AAAAGAGAAACAAATGATAT 4045
Db 1 AAAAAAAAAAAAAAAAAATTTT 24

RESULT 1622
TA155F120 24 bp DNA 1linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 155f12, reverse sequence.
ACCESSION AL472638
VERSION AL472638.1 GI:11838089
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 24)
Hall, N., Bowman, S., Lemard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .24
Location/Qualifiers

/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="155f12"

Query Match 0.2%; Score 14.4; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6977 AAAACAAACGAATGAGTGGG 7000
Db 1 AAAAAAAAAAAAAAAAAAGCGCGGG 24

RESULT 1623
AM248929 24 bp mRNA 1linear EST 07-JAN-2000
LOCUS 2819212.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819212 3',
DEFINITION mRNA sequence.
ACCESSION AM248929
VERSION AM248929.1 GI:6591922
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 24)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819212.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LBNL) DNA Sequencing by: Berkeley MGC sequencing project
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LBNL at: <http://www.bio.lbl.gov/bbrp/image/image.html> Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patchmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 10 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 24 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Place: LDCM row: A column: 5
High quality sequence stop: 10.
Location/Qualifiers
1. .24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819212"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"

FEATURES

source

/note="Organ: lung; Vector: POTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.2%; Score 14.4; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 5745 TTCTCTATCTACTCTGCTGCT 5768
Db 1 TTTTCTTTTACTCTCTTTCT 24

RESULT 1624

CF638767 25 bp mRNA linear EST 02-OCT-2003
LOCUS D06_G05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA

DEFINITION D06_G05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
ACCESSION CF638767
VERSION CF638767.1 GI:37402758
KEYWORDS EST.
SOURCE Ustilago maydis
ORGANISM Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

REFERENCE 1 (bases 1 to 25)
AUTHORS Nugent, K.G., Choffe, K. and Saville, B.J.
TITLE Euk. Expression during Ustilago maydis Diploid Filamentous Growth: EST Library Creation and Analyses
JOURNAL Unpublished (2003)
COMMENT Contact: Barry J. Saville
Saville Lab

University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utm.utoronto.ca
Plate: UTM-UM-D126/7-006-UTM row: 05 column: G
Seq primer: T7 Reverse (5' GAGTAATACACTCACTATGAGG 3')

High quality sequence stop: 25.
Location/Qualifiers
1..25

/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/note="Vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

Query Match 0.2%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 4018 AGAAAAAGAGAGAAACAAATG 4041
Db 2 AAAAAAAAAAAAAAAAAAAAAAG 25

RESULT 1625

N33150/c 25 bp mRNA linear EST 10-JAN-1996
LOCUS N33150

DEFINITION yy06g01.g1 Soares melanocyte 2NbhM Homo sapiens cDNA clone
IMAGE:270480 3' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE

(HUMAN); mRNA sequence.
ACCESSION N33150
VERSION N33150.1 GI:1153549
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 25)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1..

FEATURES

source

1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3880122"
/db_xref="taxon:9606"
/clone="IMAGE:270480"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbhM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCCCAATCGAAGTGGAGGCGCGAGTTTCTTTTCTTTTCTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 0.2%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAGAAAC 4035
Db 24 AAAAAAAAAAAAAAAAAAAAAAC 1

RESULT 1626

CF317007/c 25 bp mRNA linear EST 15-AUG-2003
LOCUS CF317007

DEFINITION HD-06-114.g1 OBHDA1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD-06-114, mRNA sequence.
ACCESSION CF317007
VERSION CF317007.1 GI:33688768
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 25)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..25
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-06-114"
 /cissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: PCR4-TOP0; Site 1: EcoRI; Callus was
 treated with ABA(20mM) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 14.4; DB 1; Length 25;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4016 TGAAGAAAAAGAGAAACAAA 4039
 Db 25 TTAATAAAAAAAAAAAAAAAAAA 2

RESULT 1627
 LOCUS TA388E06P 25 bp DNA linear GSS 13-DEC-2000
 DEFINITION genomic survey sequence.
 ACCESSION AL498782
 VERSION AL498782.1 GI:11874504
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 25)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 1..25
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="388e06"

Query Match 0.2%; Score 14.4; DB 1; Length 25;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6977 AAAACAAACGATGAGTGGG 7000
 Db 2 AAAAAAAAAAAAAAAAAAGGGGG 25

RESULT 1628
 LOCUS AZ867155 25 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0177F23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0177F23 R, genomic survey sequence.
 ACCESSION AZ867155
 VERSION AZ867155.1 GI:13069179
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0177 row: F column: 23
 Seq primer: CACACGGAACACGATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0177F23"
 /sex="Male"
 /lab_host="M". Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gt14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 4022 AAAAGAGGAAAACAAATGTTAT 4045
Db 1 AAAAAAAAAAAAAAAAAATAATAT 24

RESULT 1629

A2348233 25 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0084G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0084G04 R, genomic survey sequence.

ACCESSION A2348233
VERSION A2348233.1 GI:10427470

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0084 row: G column: 04
Seq primer: CACACGAGAAACGCTATGACC

Class: plasmid ends
High quality sequence stop: 25.

FEATURES

source

1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0084G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 3382 CTCCTCCCCAGCTGCCACCCCCC 3405
Db 2 CCCCCCCCCCACCACCCCCC 25

RESULT 1630

CF296851/c 26 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--07-G13.B1 Rice leaf plasmid cDNA library I (30DGS) Oryza

DEFINITION sativa cDNA clone 30DGS--07-G13, mRNA sequence.

ACCESSION CF296851
VERSION CF296851.1 GI:33665884

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 26)
Kim, U.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
Contact: Nahm B.H.

JOURNAL Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cullivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-G13"
/issue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 4012 AAAATGAGAAAAGAGGAAAC 4035
Db 24 AAAAAAAAAAAAAAAAAAAC 1

RESULT 1631

R26779/c 26 bp mRNA linear EST 24-APR-1995
LOCUS y144f06.81 Soares placenta Nb2HP Homo sapiens cDNA clone
DEFINITION IMAGE:13611 3' similar to gb:W85164 SERUM RESPONSE FACTOR

ACCESSION R26779
VERSION R26779.1 GI:782914

KEYWORDS EST.

SOURCE	Homio sapiens (human)
ORGANISM	Homio sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 26)
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkins, M., Holtan, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaekis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE	The Mashu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 1384 High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 1384 Std Error: 0.00 Seq primer: Promega -21m13 High quality sequence stop: 1. Location/Qualifiers 1. 26 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:538233" /db_xref="taxon:9606" /clone="IMAGE:132611" /sex="Female" /dex_stage="placenta obtained at birth (full term)" /lab_host="DH10B (ampicillin resistant)" /clone_1lb="Soares placenta Nb2HP" /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGCCGACAGAAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."
FEATURES	
source	
Query Match	0.24; Score 14.4; DB 1; Length 26;
Best Local Similarity	75.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	4016 TGAGAAAAAGAGGAAACAAA 4039
Db	24 TTAATAAAAAAAAAAAAAAAAA 1
RESULT 1632	
AZ382581/c	27 bp DNA linear GSS 02-OCT-2000
LOCUS	IM0139120R Mouse 10kb plasmid UUCIM library Mus musculus genomic
DEFINITION	clone UUCIM0139120 R, genomic survey sequence.
ACCESSION	AZ382581
VERSION	AZ382581.1 GI:10496281
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamll, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

JOURNAL
TITLE
Mouse whole genome scaffold with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: 1 column: 20
Seq primer: CACACAGCAACAGCTATGACC.
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U9C1M0139120"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U9C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.24; Score 14.4; DB 1; Length 27;
Best Local Similarity 75.04; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Gy 6977 AAAAAACAAACAGATGAGGTGGG 7000
Ddb 26 AAAAAAAAAAAAAAAAAAGGCGG 3

RESULT 1633
LOCUS TA239G06Q 29 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 239g06, reverse sequence,
genomic survey sequence.
VERSION AL481179
KEYWORDS AT481179.1 GI:11846878
SOURCE GSS.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 29)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrel, Oxford University Press, 1999).
Email: neisayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
SOURCE Location/Qualifiers
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="239906"

Query Match 0.2%; Score 14.4; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 69777 AAAAAACAACAAATGAGTGGG 7000
||||| ||||| ||||| ||||| |||||
Db 2 AAAAAAAAAAAAAAAAAAGCGGGG 25

RESULT 1634
BX557758/c 29 bp mRNA linear EST 10-OCT-2003
LOCUS BX557758 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse34e06_p1c, mRNA sequence.
BX557758
ACCESSION BX557758.1 GI:33428933
VERSION EST.
KEYWORDS Glossina morsitans morsitans
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 29)
REFERENCE Lehane,M.J., Aksoy,S., Gibson,W., Kerkhoun,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

FEATURES
SOURCE Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse34e06_p1c"
/issue_type="adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 14.4; DB 1; Length 29;
Best Local Similarity 72.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4023 AAAGAGAGAAACAAATGTTATT 4047
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Db 29 AAAAAAAAAAAAAAAAAAGCTATT 5

/db_xref="taxon:37546"
/clone="Tse34e06_p1c"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 14.4; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4020 AAAAAAGAGAAACAAATGTT 4043
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Db 29 AAAAAAAAAAAAAAAAAACTATT 6

RESULT 1635
BX561329/c 29 bp mRNA linear EST 10-OCT-2003
LOCUS BX561329 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse5b10_p1c, mRNA sequence.
BX561329
ACCESSION BX561329.1 GI:33436343
VERSION EST.
KEYWORDS Glossina morsitans morsitans
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 29)
REFERENCE Lehane,M.J., Aksoy,S., Gibson,W., Kerkhoun,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 14519198
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

FEATURES
SOURCE Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse5b10_p1c"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 14.4; DB 1; Length 29;
Best Local Similarity 72.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4023 AAAGAGAGAAACAAATGTTATT 4047
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Db 29 AAAAAAAAAAAAAAAAAAGCTATT 5

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RESULT 1636
LOCUS      AL048719
DEFINITION DKF2566G23_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL048719
VERSION     AL048719.1 GI:4727790
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE       EST (Koehrer, et al.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
FEATURES
source      Location/Qualifiers
            1..33
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKF2566G233"
            /cissue_type="kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_lib="566 (synonym: hfkd2)"
            /note="Vector: pAMP1, Site_1: NotI, Site_2: SalI"

Query Match      0.2%; Score 14.4; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      4016 TCGAAGAAAAGAGACAAACAAA 4039
        |||||
        10 TTAACAAAAAATAAAAAATAAAAA 33

RESULT 1637
LOCUS      AL047464
DEFINITION DKF2586M1320_g1 586 (synonym: hutel) Homo sapiens cDNA clone
ACCESSION  AL047464
VERSION     AL047464.1 GI:4727379
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Wamburt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE       EST (Wamburt, et al.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
FEATURES
source      Location/Qualifiers
            1..34
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKF2586M1320"
            /cissue_type="uterus"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="586 (synonym: hutel)"
            /note="Vector: pSport1, Site_1: NotI, Site_2: SalI/MluI"

Query Match      0.2%; Score 14.4; DB 1; Length 34;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      4018 AGAAAAAGAGAGAAACAAATG 4041
        |||||
        31 AAAAAAAGAGAGAGAGAGAGAGAG 8

RESULT 1638
LOCUS      AZ513919/c
DEFINITION IM0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0360E13 F, genomic survey sequence.
ACCESSION  AZ513919
VERSION     AZ513919.1 GI:10695235
KEYWORDS   GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0360 row: E column: 13
            Seq primer: CGTGTGAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES
source      Location/Qualifiers
            1..19
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0360E13"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv, Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.2%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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ACCESSION	clone UUGC1M0203011 R, genomic survey sequence.		
VERSION	A2424216		
KEYWORDS	A2424216.1 GI:10548229		
SOURCE	GSS.		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.		
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0203 row: O column: 11 Seq primer: CACACAGGAAACGCTAGACCC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers		
FEATURES	1..19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0203011" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /clone_11b="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gblAfl29072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	0.2%	Score 14.2;	DB 1; Length 19;
Best Local Similarity	84.2%;	Pred. No. 1.5e+03;	
Matches 16; Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
OY	4467	TTTTTTTTTTTTTTTTTGT	4485
Db	19	TTTGTTTTGTTTTGT	1
RESULT 1644			
A2447248	19 bp	DNA	linear GSS 04-OCT-2000
A2447248/c			
LOCUS			
DEFINITION	IM0244HH23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244H23 F, genomic survey sequence.		

ACCESSION	A2447248
VERSION	A2447248.1
KEYWORDS	GI:10599044
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C., Jellam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A., and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., STC, UT 84112, USA
COMMENT	Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0244 row: H column: 23 Seq primer: CCTGTGTAACGACGGCCACT Clase: plasmid ends High quality sequence stop: 19. Location/Qualifiers
FEATURES	1. .19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UTGCM0244H23" /sex="male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_1lb="Mouse 10kb plasmid UUGCM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
source	
Query Match	0.2%; Score 14.2; DB 1; Length 19;
Best Local Similarity	84.2%; Pred. No. 1; Se+03;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	3622 GGGGTGGGGTGGGAGAGG 3640 19 GGGGGGGGGGGGGGGGGG 1
Db	
RESULT 1645	
LOCUS	A2962226 19 bp DNA linear GSS 27-APR-2001
DEFINITION	M20231A02F Mouse 10kb plasmid UUGCM2 library Mus musculus genomic
ACCESSION	A2962226

location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0231A02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv. Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

KEYWORDS	GSS.	Mus musculus (house mouse)
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murine; Mus.	
REFERENCE	1 (bases 1 to 19)	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Isajima, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Robert B. Weis University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0231 row: P column: 08 Seq primer: CACACAGAAACACTGTGACC Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers 1. 19 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0231P08" /sex="female" /lab_host="E. coli strain XL10-Gold, TI-resistant, F-" /clone_lid="Mouse 10kb plasmid UUGC2M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
Query Match	0.28;	Score 14.2; DB 1; Length 19;
Best Local Similarity	84.28;	Pred. No. 1.5e+03;
Matches	16; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	3617	GGATGGGCTGGGCTGG 3635
Db	19	GGAAAGGGGGGGGGGG 1
RESULT 1647		
LOCUS	AZ486787/c	20 bp DNA 1linear GSS 05-OCT-2000
DEFINITION	IM0315D2JF Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315D2J F, genomic survey sequence.	
ACCESSION	AZ486787	
VERSION	AZ486787.1	GI:10653904
KEYWORDS	GSS.	

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 plate: 0315 row: D column: 23
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M031SD23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gblAf129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 4020 AAAAAAGAGAGAAAAA 4038
 ||||| ||||| ||||| |||||
 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1648
 CF340627 20 bp mRNA linear EST 18-AUG-2003
 LOCUS RCL1--08-K02.g1 Regenerated callus lambda phage cDNA library (RCL1)
 DEFINITION Oryza sativa cDNA clone RCL1--08-K02, mRNA sequence.
 ACCESSION CF340627.1 GI:33829609
 VERSION CF340627.1
 KEYWORDS EST.
 SOURCE Oryza sativa

ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim, S.S., Yun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES location/Qualifiers
 1..20
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cullivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="RCL1--08-K02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBluescript SK(+); Site 1: Sati; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with Sati and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 0.2%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.6e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 4020 AAAAAAGAGAGAAAAA 4038
 ||||| ||||| ||||| |||||
 20 AAAAAAGAGAGAAAAA 2

RESULT 1649
 AU267884 20 bp mRNA linear EST 10-MAY-2002
 LOCUS AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA
 DEFINITION AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA
 sequence.
 ACCESSION AU267884
 VERSION AU267884.1 GI:20526682
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

REFERENCE 1 (bases 1 to 20)
AUTHORS Urushihara, H., Morio, T., Saito, T., Koriiki, E., Ochiai, H., Maeda, M.,
 Takeuchi, I., Kohara, Y. and Tanaka, Y.

TITLE Population analysis of cDNAs from unicellular and multicellular
 stages of Dictyostelium discoideum

JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hideko@biol.tsukuba.ac.jp.

FEATURES location/Qualifiers
 1..20
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"


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/clone="VSH730"  
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/dev_stage="vegetative"  
/clone_lib="VS"
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Query Match	0.2%	Score 14.2;	DB 1;	length 20;
Best Local Similarity	84.2%;	Pred. No. 1.6e+03;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	4469	TTTTTTTTTTTTTTGTCCT	4487
Db	2	TTTTTTGCTTTTTCTCT	20

RESULT 1650					
AU267884/c					
LOCUS	AU267884	20 bp	mRNA	linear	EST 10-MAY-2002
DEFINITION	AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA sequence.				

ACCESSION	AU267884
VERSION	AU267884.1
KEYWORDS	GI:20526682
SOURCE	EST.
ORGANISM	<i>Dictyostelium discoideum</i>
INTERVIEW	<i>Dictyostelium discoideum</i>
	Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium

REFERENCES	Uchida S, et al. (2002)
AUTHORS	Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Tanaka, Y.
TITLE	Takeuchi, I., Kohara, Y. and Tanaka, Y.
JOURNAL	Population analysis of cDNAs from unicellular and multicellular
COMMENT	stages of <i>Dictyostellium discoideum</i>
	unpublished (2002)
	Contact: Hideko Urushihara

Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideo@biol.tsukuba.ac.jp

FEATURES	Location/Qualifiers
source	1. .20

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/organism="Dictyostellium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
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/sex="mat A"
/dev_stage="vegetative"
/clone_idb="VS"

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Query Match	0.2%	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%	Pred. NO. 1.6e+03;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

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QY      4017 GAGAAAAAAGAGAGAAAAC 4035
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Db      19 GAGAAAAAAGCAAAAAAC 1

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RESULT 1651					
BO586354					
LOCUS	BO586354	20 bp	mRNA	linear	EST 06-DEC-2007
DEFINITION	EO12395-024-013-F10-SPE MP12-ADIS-024-leaf				
DESCRIPTION	024-013-F10 5-PRIME, mRNA sequence.				Beta vulgaris cDNA clone

ACCESSION	B0586354	
VERSION	BQ586354.1	GI:26115926
KEYWORDS	EST.	
SOURCE	Beta vulgaris	
ORGANISM	Beta vulgaris	

REFERENCE
AUTHORS
Herrig, R., Schultz, B., Weishaar, B., Hennig, S., Steinfath, M.,
1 (Baese 1 to 20)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL	Plant J. 32 (5), 845-857 (2002)
	Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaasomp1z-koeln.mpg.de
Insert length: 20 Std Error: 0.00
Place: 13 low: F column: 10
Seq primer: Sp6; CATGACATTTTACGGTACACTTATAC.

FEATURES	Location/Qualifiers
SOURCE	1. .20

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/db_xref="taxon:161934"
/clone="024-013-F10"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_idb="MP12-ADIS-024-leaf"
/notes="vector: PCWSPOR6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanzielter Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPp/GABI-Primary database:http://gabi.tzpd.de"

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Query Match	0.2%	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.6e+03;		
Matches 16; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

3373	TTTGGTGTCTCTCCCC	3391
2	TTTGGGTCTCTCTCC	20

Accession	Source	Length	Insertion	Orientation	Notes
C53693	20 bp	20 bp	linear	EST 11-SEP-1997	
C53693	Yui Kohara unpublished	cdna	Caenorhabditis elegans	cdna	
	clone yk323c3 3'				mRNA sequence.

VERSION C53693.1 GI:2391450
KEYWORDS EST.
SOURCE Caenorhabditis elegans

ORGANISM *Caenorhabditis elegans*
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Pterodermidae; Caenorhabditis
1 (bases 1 to 20)
Kohara, Y., Morohashi, T., Tabara, H., Watanabe, H., Sugimoto, A.,
Sano, M., Miyata, A. and Nishigaki, A.
Expression map of the *C.elegans* genome
Unpublished (1996)
Contact: Yuji Kohara

Genome Biology Lab.
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES

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source
1. .20
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="YK323C3"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
/clone_lib="Yuji Kohara unpublished cDNA"

Query Match      0.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 6234 GCACTGTTCTTGATGTT 6252
Db 19 GCCCTGTTCTTCTGTT 1

RESULT 1653
AZ759903/c 20 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0553B11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0553B11 F, genomic survey sequence.
ACCESSION AZ759903
VERSION AZ759903.1 GI:12867167
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: B column: 11
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0553B11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to

```

```

10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor-vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 6778 CTTTACTATTGGCCTT 6796
Db 19 CTTTACAGTTTGCTT 1

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LOCUS 2M0104F03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0104F03 R, genomic survey sequence.
ACCESSION AZ827842
VERSION AZ827842.1 GI:12397750
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0104 row: F column: 03
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Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```

electroporation. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7395 TTCTGAAGCAGACATC 7413
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Db 1 TTCTGTGCAAGAACATC 19
|||||

RESULT 1655

A2835133

LOCUS

DEFINITION 20 bp DNA linear GSS 20-FEB-2001
2M0129008F Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCG2M0129008 F, genomic survey sequence.

ACCESSION A2835133
VERSION A2835133.1 GI:13005041

KEYWORDS

GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0129 row: O column: 08

Seq primer: CGTTGTAAGCAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/mol_type="genomic DNA"

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/db_xref="taxon:10090"

/clone="UGCG2M0129008"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1lb="Mouse 10kb plasmid UGCGM library"

/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

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Query Match 0.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5473 TTTTGTGTAAGATA 5491
|||||

Db 2 TTTTGTGTAAGATA 20
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RESULT 1656

A2835133/c

LOCUS

DEFINITION 20 bp DNA linear GSS 20-FEB-2001
2M0129008F Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCG2M0129008 F, genomic survey sequence.

ACCESSION A2835133
VERSION A2835133.1 GI:13005041

KEYWORDS

GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Haml, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0129 row: O column: 08

Seq primer: CGTTGTAAGCAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1lb="Mouse 10kb plasmid UGCGM library"

/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
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electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.2%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5473 TTTTGTGTAAGATGA 5491
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Db 19 TTTTGTGTAAGATGA 1

RESULT 1657
A2317208/c 21 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION IM003502R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M003502 R, genomic survey sequence.

ACCESSION A2317208 GI:10365804
VERSION
KEYWORDS
SOURCE

ORGANISM Mus musculus (house mouse)
MUS musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
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/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[g1AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4021 AAAAGGAGAGAAACAAA 4039
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Db 21 AAAAGGAGAGAAACAAA 3

RESULT 1658
A2853429 21 bp DNA linear GSS 21-FEB-2001
LOCUS
DEFINITION 2M0156D09R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0156D09 R, genomic survey sequence.

ACCESSION A2853429
VERSION
KEYWORDS
SOURCE

ORGANISM Mus musculus (house mouse)
MUS musculus

REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[g1AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4021 AAAAGAGAAACAAA 4039
DB 1 AAAAAAAAAAAAAACA 19

RESULT 1659
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LOCUS 1M0082N05F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0082N05 F, genomic survey sequence.
ACCESSION AZ346714
VERSION AZ346714.1 GI:10425951
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (baee 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0082 row: N column: 05
Seq primer: CGTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21

FEATURES
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT GT 4485
DB 21 TTTT TTTT GTATTATGT 3

RESULT 1660
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LOCUS 1M0165A23R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0165A23 R, genomic survey sequence.
ACCESSION AZ399828
VERSION AZ399828.1 GI:10514902
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (baee 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Place: 0165 row: A column: 23
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21

FEATURES
source

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/mol_type="genomic DNA"
/strain="C57BL/6J"
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

Query Match 0.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGGTGGGAGAGG 3640
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Db 20 GGGGTGGGATGGGTAAAG 2

RESULT 1663
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LOCUS
DEFINITION 2M0004G14F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGM0004G14 F, genomic survey sequence.
ACCESSION AZ774703
VERSION AZ774703.1 GI:1290261
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
TEL: 801 585 5606
FAX: 801 585 7177
EMAIL: ddunn@genetics.utah.edu
INSERT LENGTH: 10000 Std Error: 0.00
PLACE: 0004 row: G column: 14
SEQ PRIMER: CGTGTAAACGACGCCACGT
CLASS: plasmid ends
High quality sequence stop: 21.

FEATURES

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3622 GGGGTGGGGGTGGGAGAGG 3640
|||||
Db 20 GGGGGGGGGGTGGGGGGG 2

RESULT 1664
AZ809249 21 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION 2M0073112F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGM0073112 F, genomic survey sequence.
ACCESSION AZ809249
VERSION AZ809249.1 GI:12975387
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
UNIVERSITY OF UTAH Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
TEL: 801 585 5606
FAX: 801 585 7177
EMAIL: ddunn@genetics.utah.edu
INSERT LENGTH: 10000 Std Error: 0.00
PLACE: 0073 row: T column: 12
SEQ PRIMER: CGTGTAAACGACGCCACGT
CLASS: plasmid ends
High quality sequence stop: 21.

FEATURES

1.21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0073112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

0.2%; Score 14.2; DB 1; Length 21;

Best Local Similarity 84.2%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4467 TTTTGTGTGTGTGTGT 4485
Db 2 TTTGTGTGTGTGTGTGT 20

RESULT 1665
AZ936997 21 bp DNA linear GSS 26-APR-2001
LOCUS AZ936997
DEFINITION 2M0195H01F Mouse 10kb plasmid UGCC2M library Mus musculus genomic
clone UGCC2M0195H01 F, genomic survey sequence.
ACCESSION AZ936997
VERSION AZ936997.1 GI:13795578
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mamoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0195 row: H column: 01
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UGCC2M0195H01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus CS7BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1|4732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 1.8e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 774 CCACCCGCTGGGGGCTGGG 792
Db 2 CTTCCCTGGGGGGGGGG 20

RESULT 1666
CF313297/c 23 bp mRNA linear EST 15-AUG-2003
LOCUS CF313297
DEFINITION HD-01-G01.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD-01-G01, mRNA sequence.
ACCESSION CF313297
VERSION CF313297.1 GI:33685058
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-01-G01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E. coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 14.2; DB 1; Length 23;
Best Local Similarity 84.2%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4021 AAAAAAGAGAAAAA 4039
Db 20 AAAAAAGAAAAA 2
RESULT 1667
AZ984045/c 23 bp DNA linear GSS 27-APR-2001
LOCUS AZ984045
DEFINITION 2M0265I23F Mouse 10kb plasmid UGCC2M library Mus musculus genomic
clone UGCC2M0265I23 F, genomic survey sequence.
ACCESSION AZ984045
VERSION AZ984045.1 GI:13855272
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers

1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-009"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14.2; DB 1; Length 27;
Best Local Similarity 70.4%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4012 AAATGAGAAAAAGAGAAACAAA 4038
Db 27 AAAAAAAAAATTTAAAAA 1

RESULT 1670
TR165H05P/c 27 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 165h05, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL472045
VERSION AL472045.1 GI:11837399
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source location/Qualifiers

1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="165h05"

Query Match 0.2%; Score 14.2; DB 1; Length 27;
Best Local Similarity 70.4%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4032 AACCAAAATGTTATTTATACATTA 4058
Db 27 AAAAAAAAACTTTTTTAAAAA 1

RESULT 1671
CF277114/c 28 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--02-111.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa cDNA clone 14ETL--02-111, mRNA sequence.
ACCESSION CF277114
VERSION CF277114.1 GI:33654500
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatroidae; Oryzaceae; Oryza.
1 (bases 1 to 28)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source location/Qualifiers

1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--02-111"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14.2; DB 1; Length 28;
Best Local Similarity 84.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4021 AAAAAAGAGAAAAA 4039
Db 21 AAAAAAGAAAAA 3

RESULT 1672
BX554068/c 31 bp mRNA linear EST 10-OCT-2003
LOCUS BX554068 Glosina morsitans morsitans adult infected gut Glosina
DEFINITION morsitans morsitans cDNA clone Tse13c01_pic, mRNA sequence.
ACCESSION BX554068
VERSION BX554068.1 GI:33378169
KEYWORDS EST.
SOURCE Glosina morsitans morsitans
ORGANISM Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glosina.

FEATURES
source location/Qualifiers

REFERENCE 1 (bases 1 to 31)
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M.,
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES
 source Location/Qualifiers
 1..31
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse32f01_p1c"
 /issue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4021 AAAAGAGGAAACAAATGTTATT 4047
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1673
 BXS57470/c 31 bp mRNA linear EST 10-OCT-2003
 LOCUS BXS57470 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse32f01_p1c, mRNA sequence.
 ACCESSION BXS57470
 VERSION BXS57470.1 GI:33428655
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.
 1 (bases 1 to 31)
 Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
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 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW

REFERENCE 1 (bases 1 to 31)
 AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M.,
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
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 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES
 source Location/Qualifiers
 1..31
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse32f01_p1c"
 /issue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4021 AAAAGAGGAAACAAATGTTATT 4047
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1674
 BXS58479/c 31 bp mRNA linear EST 10-OCT-2003
 LOCUS BXS58479 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse32f01_p1c, mRNA sequence.
 ACCESSION BXS58479
 VERSION BXS58479.1 GI:33365232
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.
 1 (bases 1 to 31)
 Lehane,M.J., Aksoy,S., Gibson,W., Kexhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW

Query Match 0.2%; Score 14.2; DB 1; Length 31;
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4021 AAAAAGAGAAAACAAATGTTATTT 4047
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1675
 EX559254/c 31 bp mRNA linear EST 10-OCT-2003
 LOCUS BX559254 Glossina morsitans morsitans adult infected gut Glossina
 DEFINITION morsitans morsitans cDNA clone Tse42e03_p1c, mRNA sequence.
 ACCESSION BX559254
 VERSION BX559254.1 GI:33366605
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 31)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
 response genes
 Genom. Biol. 4 (10), R63 (2003)

JOURNAL MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all pic reads are from
 the 3' end.

FEATURES
 source Location/Qualifiers
 1..31
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse42e03_p1c"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 31;
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4021 AAAAAGAGAAAACAAATGTTATTT 4047
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1676
 BX551100 32 bp mRNA linear EST 10-OCT-2003
 LOCUS BX551100 Glossina morsitans morsitans adult infected gut Glossina
 DEFINITION morsitans morsitans cDNA clone Tse116f01_p1c, mRNA sequence.
 ACCESSION BX551100
 VERSION BX551100.1 GI:33374951
 KEYWORDS EST.

SOURCE
 ORGANISM Glossina morsitans morsitans
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 32)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
 response genes
 Genom. Biol. 4 (10), R63 (2003)

JOURNAL MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all pic reads are from
 the 3' end.

FEATURES
 source Location/Qualifiers
 1..32
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse116f01_p1c"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 32;
 Best Local Similarity 70.4%; Pred. No. 2.3e+03;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4021 AAAAAGAGAAAACAAATGTTATTT 4047
 Db 31 AAAAAAAAAAAAAAAAAAACTATCT 5

RESULT 1677
 BX553142 33 bp mRNA linear EST 10-OCT-2003
 LOCUS BX553142 Glossina morsitans morsitans adult infected gut Glossina
 DEFINITION morsitans morsitans cDNA clone Tse127f01_p1c, mRNA sequence.
 ACCESSION BX553142
 VERSION BX553142.1 GI:33377335
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 33)
 Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly *Glossina*
morsitans morsitans and expression analysis of putative immune
 response genes
 Genom. Biol. 4 (10), R63 (2003)

JOURNAL MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qtc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source

Location/Qualifiers
1. .33
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse127101_plc"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 14.2; DB 1; Length 33;
Best Local Similarity 70.4%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4021 AAAAGAGGAAACAAATGTTATT 4047

Db 31 AAAAAAAAAAAAAAAAAAACTACT 5

RESULT 1678

LOCUS AZ861400 35 bp DNA linear GSS 21-FEB-2001
DEFINITION ZM0167013R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCGM0167013 R, genomic survey sequence.

ACCESSION AZ861400

VERSION

KEYWORDS

SOURCE

ORGANISM

MUS musculus (house mouse)

MUS musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0167 row: 0 column: 13
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1. .35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0167013"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42n; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi4732114|gb1AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 14.2; DB 1; Length 35;
Best Local Similarity 62.9%; Pred. No. 2.2e+03;
Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 33 CTGCTGCGAGCTCCGCGGCGGCGACGAGCT 67

Db 35 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

RESULT 1679

LOCUS BQ586422 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S01307-024-013-002-T7 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-002 3-PRIME, mRNA sequence.

ACCESSION BQ586422

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mplz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 13 row: 0 column: 02
Seq primer: T7; GTATACGACCTACTATAGGAC.
Location/Qualifiers
1. .14
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186441"
/db_xref="taxon:161934"
/clone="024-013-002"
/issue_type="leaf"
/lab_host="EMDH108"
/clone_lib="MP12-ADIS-024-leaf"

/note=Vector: PCWVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Bindeck, Germany; contact:
b.schulz@kws.de; Cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1680

BO587890

LOCUS BO587890 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S013302-024-009-B02-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-009-B02 3-PRIME, mRNA sequence.

ACCESSION BO587890
VERSION BO587890.1 GI:26117472
KEYWORDS EST.

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PubMed 12472698

COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
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Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 14 Std Error: 0.00
Plate: 9 row: B column: 02
Seq primer: T7; GTATACGACTCCTATTAAGGC.
Location/Qualifiers

FEATURES

source

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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
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/issue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note=Vector: PCWVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Bindeck, Germany; contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1681

BO589191

LOCUS BO589191 14 bp mRNA linear EST 06-DEC-2002
DEFINITION S014009-024-015-120-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-015-120 3-PRIME, mRNA sequence.

ACCESSION BO589191
VERSION BO589191.1 GI:26118774
KEYWORDS EST.

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PubMed 12472698

COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
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Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 14 Std Error: 0.00
Plate: 15 row: I column: 20
Seq primer: T7; GTATACGACTCCTATTAAGGC.
Location/Qualifiers

FEATURES

source

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/issue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note=Vector: PCWVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Bindeck, Germany; contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1682
 BQ590242 14 bp mRNA linear EST 06-DEC-2002
 LOCUS E012840-024-019-E16-SP6 MP12-ADIS-024-storage root Beta vulgaris
 DEFINITION CDNA clone 024-019-E16 5-PRIME, mRNA sequence.
 ACCESSION BQ590242
 VERSION BQ590242.1 GI:26119825
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 14)
 Hwang, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
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 ADIS DNA core facility at MP1Z
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 Fax: 00492215062851
 Email: weishaar@mp1z-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
 Plate: 19 row: E column: 16
 Seq primer: SP6; CATACGATTAGTCACACTATAG.
 Location/Qualifiers
 1. 14
 /organism="Beta vulgaris"
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 /clone="024-019-E16"
 /cissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: PCWVS-PORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4477
 DB 1 TTTT TTTT TTTT TTTT 14

RESULT 1683
 BQ590261 14 bp mRNA linear EST 06-DEC-2002
 LOCUS E012844-024-019-K14-T7 MP12-ADIS-024-storage root Beta vulgaris
 DEFINITION CDNA clone 024-019-K14 3-PRIME, mRNA sequence.
 ACCESSION BQ590261
 VERSION BQ590261.1 GI:26119844
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 14)
 Hwang, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698
 COMMENT Contact: Weishaar B
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 Max-Planck-Institute for Plant Breeding Research
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 Fax: 00492215062851
 Email: weishaar@mp1z-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
 Plate: 19 row: K column: 14
 Seq primer: T7; GTAATACGACTCATATAGCGC.
 Location/Qualifiers
 1. 14
 /organism="Beta vulgaris"
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 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="taxon:161934"
 /clone="024-019-K14"
 /cissue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: PCWVS-PORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCACGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by R2PD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT 4477
 DB 1 TTTT TTTT TTTT TTTT 14

RESULT 1684
 BQ591168 14 bp mRNA linear EST 06-DEC-2002
 LOCUS E012715-024-017-H18-T7 MP12-ADIS-024-storage root Beta vulgaris
 DEFINITION CDNA clone 024-017-H18 3-PRIME, mRNA sequence.
 ACCESSION BQ591168
 VERSION BQ591168.1 GI:26120751
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 14)
 Hwang, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189
PubMed 12472698
COMMENT Contact: Weishaar B
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Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: H column: 18
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .14
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line)"
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/lab_host="EMD10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanzelebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1685
BOS91176 14 bp mRNA linear EST 06-DEC-2002
LOCUS E012715-024-017-N20-T7 MPiZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-N20 3-PRIME, mRNA sequence.
ACCESSION BOS91176
VERSION BOS91176.1 GI:26120759
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
Insert Length: 14 Std Error: 0.00
Plate: 17 row: N column: 20

TITLE
JOURNAL
MEDLINE
PubMed
COMMENT Contact: Weishaar B
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Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: N column: 20

Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
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line)"
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/clone="024-017-N20"
/issue_type="storage root"
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/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanzelebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1686
BOS91207 14 bp mRNA linear EST 06-DEC-2002
LOCUS E012715-024-017-B04-T7 MPiZ-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-B04 3-PRIME, mRNA sequence.
ACCESSION BOS91207
VERSION BOS91207.1 GI:26120790
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 04
Seq primer: T7; GTAATACGACTCACTATAGGCG.
Location/Qualifiers
1. .14
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultiVar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188904"
/db_xref="taxon:161934"
/clone="024-017-B04"

TITLE
JOURNAL
MEDLINE
PubMed
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPiZ
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Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 14 Std Error: 0.00
Plate: 17 row: B column: 04

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cDNA library from sugar beet, library provided by KWS
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b.schulz@kws.de; cloning sites Sali-Notti, primer sites and
orientation:
SP6-Sali-CCACGCGCTCCG-5prime-cDNA-polyA-CC-Notti-T7; Note:
Sequencing granted in the context of the GABI-BeeT
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
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Qy      4464 TTTTTTTTTTTTTT 4477
Db      1 TTTTTTTTTTTTTT 14

RESULT 1687
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LOCUS      E012713-024-017-B15-T7 MP12-ADIS-024-storage root Beta vulgaris
DEFINITION      cDNA clone 024-017-B15 3-PRIME, mRNA sequence.
ACCESSION      BOS91380
VERSION      BOS91380.1 GI:26120963
KEYWORDS      EST.
SOURCE      Beta vulgaris
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,D., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED      12472698
COMMENT      Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Location/Qualifiers
1. 14
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cDNA library from sugar beet, library provided by KWS
Kleinanleberener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-Notti, primer sites and
orientation:
SP6-Sali-CCACGCGCTCCG-5prime-cDNA-polyA-CC-Notti-T7; Note:
Sequencing granted in the context of the GABI-BeeT
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source

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project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTTTTTTTTTTTT 4477
Db      1 TTTTTTTTTTTTTT 14

RESULT 1688
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LOCUS      E012713-024-017-M04-T7 MP12-ADIS-024-storage root Beta vulgaris
DEFINITION      cDNA clone 024-017-M04 3-PRIME, mRNA sequence.
ACCESSION      BOS91482
VERSION      BOS91482.1 GI:26121065
KEYWORDS      EST.
SOURCE      Beta vulgaris
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 14)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,D., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED      12472698
COMMENT      Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert length: 14 Std Error: 0.00
Plate: 17 row: M column: 04
Seq primer: T7; GATATACGATCCTACTATAGGCG.
Location/Qualifiers
1. 14
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line)"
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cDNA library from sugar beet, library provided by KWS
Kleinanleberener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-Notti, primer sites and
orientation:
SP6-Sali-CCACGCGCTCCG-5prime-cDNA-polyA-CC-Notti-T7; Note:
Sequencing granted in the context of the GABI-BeeT
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source

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Db 1 TTTT TTTT TTTT 14

RESULT 1689

LOCUS B0593052 14 bp mRNA linear EST 06-DEC-2002

DEFINITION E012375-024-028-C03-SP6 MP1Z-ADIS-024-developing root Beta vulgaris

ACCESSION B0593052

VERSION B0593052.1 GI:26122635

KEYWORDS EST.

ORGANISM Beta vulgaris

REFERENCE Beta vulgaris

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

COMMENT Contact: Weishaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 28 row: C column: 03

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzehnlebeener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZP/GABI-Primary database: <http://gabi.rzp.de>"

Query Match 0.2%; Score 14; DB 1; Length 14;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT 4477

1 TTTT TTTT TTTT 14

RESULT 1690

LOCUS CF277935 14 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL-03-K11 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF277935

VERSION CF277935.1 GI:33655321

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT 14

RESULT 1691

LOCUS CF278001 14 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL-03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION CF278001

VERSION CF278001.1 GI:33655387

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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Query Match 0.2%; Score 14; DB 1; Length 14;
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Qy 4464 TTTT TTTT TTTT TTTT 4477
 1 TTTT TTTT TTTT TTTT 14

RESULT 1692
 CF278452

LOCUS CF278452 14 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 ACCESSION CF278452
 VERSION CF278452.1 GI:33655838
 KEYWORDS EST.

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 1 TTTT TTTT TTTT TTTT 14

RESULT 1693
 CF279473
 LOCUS CF279473 14 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 ACCESSION Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
 VERSION CF279473
 KEYWORDS CF279473.1 GI:33656859
 SOURCE EST.
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 SOURCE Location/Qualifiers
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RESULT 1694
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LOCUS CF279992 14 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 ACCESSION Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
 VERSION CF279992
 KEYWORDS CF279992.1 GI:33657378
 SOURCE EST.

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 SOURCE Location/Qualifiers

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

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Query Match 0.2%; Score 14; DB 1; Length 14;
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Oy 4464 TTTTTTTTTTTT 4477
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RESULT 1698

CF295570

LOCUS CF295570 14 bp mRNA linear EST 14-AUG-2003
 DEFINITION 30DS--05-J06.g1 Rice leaf plasmid cDNA library I (30DS) Oryza
 ACCESSION CF295570
 VERSION CF295570.1 GI:33664603
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

1 (bases 1 to 14)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

source

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 /clone_1ib="Rice leaf plasmid cDNA library I (30DS)"
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Oy 4464 TTTTTTTTTTTT 4477
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Db 1 TTTTTTTTTTTT 14

RESULT 1699

CF296120

LOCUS CF296120 14 bp mRNA linear EST 14-AUG-2003
 DEFINITION 30DS--06-F17.b1 Rice leaf plasmid cDNA library I (30DS) Oryza
 ACCESSION CF296120
 VERSION CF296120.1 GI:33665153
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

1 (bases 1 to 14)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.
 Location/Qualifiers

FEATURES

source

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 |||||
 1 TTTTTTTTTTTT 14

RESULT 1700

CF297969

LOCUS CF297969 14 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 ACCESSION CF297969
 VERSION CF297969.1 GI:33669730
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.

1 (bases 1 to 14)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, Y.-K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division
 of Bioscience and Bioinformatics, Myongji University

Query Match 0.2%; Score 14; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTTTTTTTTTT 4477
 |||||

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

1. .14
/organism="Oryza sativa"
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TTTT TTTT TTTT TTTT 14

RESULT 1701

CF298109 14 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CP298109
VERSION CP298109.1 GI:33669870
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

SOURCE

1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/dev_stage="7 days after germination"
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/note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1702

CF299368 14 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CP299368
VERSION CP299368.1 GI:33671129
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

SOURCE

1. .14
/organism="Oryza sativa"
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QY 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

RESULT 1703

CF300542 14 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION
ACCESSION CF300542
VERSION CF300542.1 GI:33672303
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

REFERENCE
AUTHORS
TITLE
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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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1. .14
Location/Qualifiers

/organism="Oryza sativa"
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Oy 4464 TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1704
CF301020 14 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--05-L10, mRNA sequence.

ACCESSION CF301020
VERSION CF301020.1 GI:33672781

KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers

/organism="Oryza sativa"
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Query Match 0.2%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

RESULT 1705

CF301083 14 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--05-M19, mRNA sequence.

ACCESSION CF301083
VERSION CF301083.1 GI:33672844

KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .14
Location/Qualifiers

/organism="Oryza sativa"
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Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1706

CF301380 14 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-D16, mRNA sequence.

ACCESSION CF301380
VERSION CF301380.1 GI:33673141

KEYWORDS EST.
SOURCE Oryza sativa

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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1. .14
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
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Oy 4464 TTTT TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1707
LOCUS CF302675 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-G18 b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF302675
VERSION CF302675.1 GI:33674436
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
SOURCE
1. .14
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/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1708
LOCUS CF302846 14 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--08-M05 b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF302846
VERSION CF302846.1 GI:33674607
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
SOURCE
1. .14
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4477
|||||
1 TTTT TTTT TTTT TTTT 14

RESULT 1709
LOCUS CF308006 14 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--01-K10 g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.
ACCESSION CF308006
VERSION CF308006.1 GI:33679767
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1710

LOCUS

CF308220 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.

ACCESSION

CF308220

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1.14

/organism="Oryza sativa"

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FEATURES

source

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1711

LOCUS

CF308445 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.

ACCESSION

CF308445

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

AUTHORS

TITLE

JOURNAL

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1.14

/organism="Oryza sativa"

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line."

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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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SOURCE
ORGANISM
Oryza sativa

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.

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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (ABF)"
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element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1713
CF310714 14 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--05-111.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-111, mRNA sequence.
CF310714
VERSION
CF310714.1 GI:33682475
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

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Tel: 82 31 330 6193
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

/cultivar="Nackdong"
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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1714
CF311201 14 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.
CF311201
VERSION
CF311201.1 GI:33682962
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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FEATURES
source
1. .14
/organism="Oryza sativa"
/mol_type="mRNA"
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cDNA library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

RESULT 1715

CF31813

LOCUS CF31813 14 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.

ACCESSION CF31813

VERSION CF31813.1 GI:33683574

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Location/Qualifiers

FEATURES

source

1..14

/organism="Oryza sativa"

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cDNA library (ABF)"

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element binding transcription factor 3 overexpression

line."

Query Match 0.2%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 1716

CF318323

LOCUS CF318323 14 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--08-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-G13, mRNA sequence.

ACCESSION CF318323

VERSION CF318323.1 GI:33690084

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Fax: 82 31 321 6355
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Location/Qualifiers

FEATURES

source

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/organism="Oryza sativa"

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/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid

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/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was

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derived from rice Histone Deacetylase overexpression

line."

Query Match 0.2%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 1717

CF318450

LOCUS CF318450 14 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--08-J08.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.

ACCESSION CF318450

VERSION CF318450.1 GI:33690211

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

source

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

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/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO, Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression
line."

Query Match 0.2%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1718

CF319826

LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-10-H16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD-10-H16, mRNA sequence.
CF319826

ACCESSION CF319826.1 GI:33691587

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretidoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Location/Qualifiers

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

/culivar="Nackdong"

/db_xref="taxon:4530"

/clone="HD-10-H16"

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/clone_1lb="OSHDA1-overexpressing transgenic rice plasmid

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/note="Vector: PCR4-TOP0; Site 1: EcoRI; Callus was

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reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.2%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

RESULT 1719

CF321246

LOCUS 14 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-12-G24.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD-12-G24, mRNA sequence.
CF321246

ACCESSION CF321246.1 GI:33693007

VERSION EST.

KEYWORDS

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretidoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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Location/Qualifiers

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

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/db_xref="taxon:4530"

/clone="HD-12-G24"

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/dev_stage="proliferated callus on 2N6 media for 2 weeks"

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/clone_1lb="OSHDA1-overexpressing transgenic rice plasmid

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/note="Vector: PCR4-TOP0; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT 4477
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1 TTTT TTTT TTTT TTTT 14

RESULT 1720

CF327097

LOCUS 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL-01-H01.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL-01-H01, mRNA sequence.
CF327097

ACCESSION CF327097.1 GI:33802449

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehretidoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Email: bhnaheg@bio.com, bhnaheg@bio.myongji.ac.kr.

Location/Qualifiers

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

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Query Match 0.2%; Score 14; DB 1; Length 14;
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OY 4464 TTTT TTTT TTTT TTTT 4477
 1 TTTT TTTT TTTT TTTT 14

RESULT 1721

CF327119

LOCUS CF327119 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-H14, mRNA sequence.

ACCESSION CF327119

VERSION CF327119.1 GI:33802493

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

JOURNAL Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

COMMENT

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FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

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RT-PCR."

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OY 4464 TTTT TTTT TTTT TTTT 4477
 1 TTTT TTTT TTTT TTTT 14

RESULT 1722

CF327203

LOCUS CF327203 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-J16, mRNA sequence.

ACCESSION CF327203
 VERSION CF327203.1 GI:33802665
 KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

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 Yongin, Kyeonggi, Korea
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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..14

/organism="Oryza sativa"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1723

CF327445

LOCUS CF327445 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--01-O24, mRNA sequence.

ACCESSION CF327445

VERSION CF327445.1 GI:33803149

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

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 of BioScience and Bioinformatics, Myongji University
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 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Location/Qualifiers

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/organism="Oryza sativa"

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OY 4464 TTTT TTTT TTTT TTTT 4477
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 1 TTTT TTTT TTTT TTTT 14

RESULT 1724

LOCUS CF328490 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--03-G21, mRNA sequence.

ACCESSION CF328490
 VERSION CF328490.1 GI:33805226
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

CONTACT: Nahm B.H.

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 of Bioscience and Bioinformatics, Myongji University
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 Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

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Query Match 0.2%; Score 14; DB 1; Length 14;
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RESULT 1725

LOCUS CF328540 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--03-H24, mRNA sequence.

ACCESSION CF328540
 VERSION CF328540.1 GI:33805324
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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 Unpublished (2003)

CONTACT: Nahm B.H.

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Location/Qualifiers

FEATURES

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Query Match 0.2%; Score 14; DB 1; Length 14;
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OY 4464 TTTT TTTT TTTT TTTT 4477
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RESULT 1726

LOCUS CF328669 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--03-K23, mRNA sequence.

ACCESSION CF328669
 VERSION CF328669.1 GI:33805587
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)
 Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

CONTACT: Nahm B.H.

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Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

SOURCE

1..14
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RT-PCR."

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RESULT 1727
 LOCUS CF328994 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--04-C11.D1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--04-C11, mRNA sequence.
 ACCESSION CF328994
 VERSION CF328994.1 GI:33806228
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)

TITLE JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
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 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RESULT 1728
 LOCUS CF329217 14 bp mRNA linear EST 18-AUG-2003

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DEFINITION NACL--04-H10.D1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-H10, mRNA sequence.
ACCESSION CF329217
VERSION CF329217.1 GI:33806672
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

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REFERENCE 1 (bases 1 to 14)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RESULT 1729
 LOCUS CF329990/c 14 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--05-111.G1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--05-111, mRNA sequence.
 ACCESSION CF329990
 VERSION CF329990.1 GI:33808202
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 14)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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 Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RESULT 1730
CF330784 14 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--06-K10, mRNA sequence.
ACCESSION CF330784
VERSION CF330784.1 GI:33809790
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)

TITLE Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

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RESULT 1731
CF331272

LOCUS CF331272 14 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331272
VERSION CF331272.1 GI:33810755
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

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RESULT 1732

CF331861 14 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--08-C10, mRNA sequence.
ACCESSION CF331861
VERSION CF331861.1 GI:33811945
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Unpublished (2003)
JOURNAL Contact: Nahm B.H.
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers

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Db

RESULT 1733
CF333214 14 bp mRNA linear EST 18-AUG-2003
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DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION CF333214
VERSION CF333214.1 GI:33814707
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
location/Qualifiers
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prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

RESULT 1733
CF333215/c 14 bp mRNA linear EST 18-AUG-2003
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DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-A10, mRNA sequence.
ACCESSION CF333215
VERSION CF333215.1 GI:33814709
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
location/Qualifiers
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/organism="Oryza sativa"
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1 TTTT TTTT TTTT TTTT 14
Db

RESULT 1735
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LOCUS JMT--02-E12.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

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Db

RESULT 1735
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LOCUS JMT--02-E12.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-E12, mRNA sequence.
ACCESSION CF333399
VERSION CF333399.1 GI:33815074
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1. .14
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Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 1736

CF334202 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.
ACCESSION CF334202
VERSION CF334202.1 GI:33816736
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

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CDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4477
1 TTTT TTTT TTTT TTTT 14

RESULT 1737

CF334281 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--03-105.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-105, mRNA sequence.
ACCESSION CF334281
VERSION CF334281.1 GI:33816894
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

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CDNA library (JMT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT 4477
1 TTTT TTTT TTTT TTTT 14

RESULT 1738

CF334290 14 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--03-111.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-111, mRNA sequence.
ACCESSION CF334290
VERSION CF334290.1 GI:33816914
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.
1 (bases 1 to 14)

REFERENCE

1 (bases 1 to 14)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
TITLE Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
 Contact: Nahm, B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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 prepared from Arabidopsis Jasmonate Carboxyl
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Query Match
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
 |||||
 1 TTTT TTTT TTTT 14

RESULT 1739

LOCUS CF335781 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--05-J13.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.
ACCESSION CF335781
VERSION CF335781.1 GI:33819936
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 14)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm, B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
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 1 TTTT TTTT TTTT 14

RESULT 1740
LOCUS CF336094 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-A10.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.
ACCESSION CF336094
VERSION CF336094.1 GI:33820566
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 14)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm, B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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 /dev_stage="14 days after germination"
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 cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
 |||||
 1 TTTT TTTT TTTT 14

RESULT 1741
LOCUS CF336106 14 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--06-A17.b1 AtUMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.
ACCESSION CF336106
VERSION CF336106.1 GI:33820590


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KEYWORDS      EST.
SOURCE         Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Eubacteriobacteriota; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
TITLE          Unpublished (2003)
JOURNAL        Contact: Nahm B.H.
COMMENT        Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongsin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                Location/Qualifiers
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                /dev_stage="14 days after germination"
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                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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                prepared from Arabidopsis thymosinase Carboxyl
                methyltransferase overexpression line."

Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT 4477
          |||||
          1 TTTT TTTT TTTT TTTT 14

Db
1 TTTT TTTT TTTT TTTT 14

RESULT 1742
CE336287      14 bp mRNA linear EST 18-AUG-2003
DEFINITION    JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
                library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.
ACCESSION     CE336287
VERSION       CE336287.1 GI:33820962
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Eubacteriobacteriota; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
TITLE          Unpublished (2003)
JOURNAL        Contact: Nahm B.H.
COMMENT        Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongsin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                Location/Qualifiers
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Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT 4477
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Db
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis thymosinase Carboxyl
methyltransferase overexpression line."

Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT 4477
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Db
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methyltransferase overexpression line."

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methyltransferase overexpression line."

Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT 4477
          |||||
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Db
1 TTTT TTTT TTTT TTTT 14

RESULT 1743
CE336906      14 bp mRNA linear EST 18-AUG-2003
DEFINITION    JMT--07-C05.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
                library (JMT) Oryza sativa cDNA clone JMT--07-C05, mRNA sequence.
ACCESSION     CE336906
VERSION       CE336906.1 GI:33822182
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Eubacteriobacteriota; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                Large-scale Sequencing Analysis of Rice ESTs
                Unpublished (2003)
TITLE          Unpublished (2003)
JOURNAL        Contact: Nahm B.H.
COMMENT        Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongsin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
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Qy      4464 TTTT TTTT TTTT TTTT 4477
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Db
1 TTTT TTTT TTTT TTTT 14

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prepared from Arabidopsis thymosinase Carboxyl
methyltransferase overexpression line."

Query Match      0.2%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT 4477
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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prepared from Arabidopsis thymosinase Carboxyl
methyltransferase overexpression line."

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RESULT 1744
CF295100 15 bp mRNA linear EST 14-AUG-2003
LOCUS 30DS--04-002.b1 Rice leaf plasmid cDNA library I (30DS) Oryza
DEFINITION Bativa cDNA clone 30DS--04-002, mRNA sequence.
ACCESSION CF295100
VERSION CF295100.1 GI:33664133
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 1745
CF329379 15 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--04-K23, mRNA sequence.
ACCESSION CF329379
VERSION CF329379.1 GI:33806995
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355

FEATURES
source
1..15
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
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Db 16 TTTT TTTT TTTT TTTT 3

RESULT 1746
CF291803 16 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION CF291803
VERSION CF291803.1 GI:33660836
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhacridae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..16
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-G05"
/issue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
|||||
Db 16 TTTT TTTT TTTT TTTT 3

```

RESULT 1747
LOCUS      AM250784              17 bp    mRNA       linear   EST-07-JAN-2000
DEFINITION 2822335.3prine NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822335 3'.
ACCESSION  AM250784
VERSION     AM250784
KEYWORDS    GI:6593777
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 17)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other ESTs: 2822335.5prine
            Contact: Robert Strausberg, Ph.D.
            Email: cga@pb.t-e@mail.nih.gov
            Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
            Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (ILN). DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/ILN at:
            www-bio.lnlnl.gov/btbp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from university of Washington Genome Center
            PRRAP suite. Poly-T identification: patmatch.pl from Berkeley
            Dirosophila Genome Project. Univversity of Washington Genome Center::
            http://www.genome.washington.edu low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence.
            Plate: LHCMS row: C column: 8.
FEATURES             Location/Qualifiers
     source           1..17
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822335"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_id="NIH_MGC_7"
                     /note="Organ: lung; Vector: pORF7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'-
                     adaptor: GGGACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
Query Match      0.2%; Score 14; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY               4464 TTTTTCCTTTTTCCTTTTCCTT 4460
                   |||||
Db                1 TTNNNTTTTTCCTTTTCCTT 17

RESULT 1748
LOCUS      CF339347              17 bp    mRNA       linear   EST-18-AUG-2003
DEFINITION  RC1L--04-013.g1 Regenerated callus lambda phage cDNA library (RC1L)
ACCESSION  CF339347
VERSION     CF339347
KEYWORDS    GI:33827081
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
```

REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 17) Kim,J.-S., Jun,K.M., Cheong,P.-J., Kim,M.-J., Lee,T.H., Shin,Y.C., Song,S.-I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES	Location/Qualifiers
source	1..17 /organism="Oryza sativa" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:4530" /clone="RCL1--04-J13" /tissue_type="callus" /dev_stage="proliferated callus on 2N6 media for 30 days" /lab_host="E.coli SOLR" /clone_lib="Regenerated callus lambda phage cDNA library (RCL1)" /note="Vector: pBluescript SK(+); Site_1: SstI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"
Query Match	0.2%; Score 14; DB 1; Length 17;
Best Local Similarity	100.0%; Pred. No. 1.3e+03;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ox	5707 CCTTTCCTCTCT 5720 4 CCTTTCCTCTCT 17
RESULT 1749	
LOCUS	AM249856 18 bp mRNA linear EST 07-JAN-2000
DEFINITION	2821566.3xpriime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821566 3', mRNA sequence.
ACCESSION	AM249856
VERSION	AM249856.1 GI:6592849
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 18) NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Unpublished (1999)
JOURNAL	Other ESTs: 2821566.5xpriime
COMMENT	Contact: Robert Strausberg, Ph.D. Email: gsabbs-remail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Fubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: www.bio.lnl.ni.gov/dbp/Image/Image.html Base Calling / Quality Scores: PHRD from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRD high quality bases following vector sequence. Very Low

Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM row: C column: 7 High quality sequence stop: 9. Location/Qualifiers

FEATURES

source

1.18
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:2821566"
/issue_type="small cell carcinoma"
/cell_line="MG3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="N1H_MGC_7"
/note="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match
Best Local Similarity 93.3%; Score 14; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4470 TTTT TTTT TTTT TTTT G 4484
|||||
Db 1 TTTT TTTT TTTT TTTT G 15

RESULT 1750

AZ856873 19 bp DNA linear GSS 21-FEB-2001
LOCUS AZ856873
DEFINITION 2M0161019F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0161019 F, genomic survey sequence.

ACCESSION AZ856873
VERSION AZ856873.1 GI:13048296
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: O column: 19
Seq primer: CGTGTGAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UGCG2M0161019"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 100.0%; Score 14; DB 1; Length 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT T 4477
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Db 1 TTTT TTTT TTTT TTTT T 14

RESULT 1751

AZ950028 19 bp DNA linear GSS 27-APR-2001
LOCUS AZ950028/c
DEFINITION 2M0213119R Mouse 10kb plasmid UGCG2M library Mus musculus genomic
clone UGCG2M0213119 R, genomic survey sequence.

ACCESSION AZ950028
VERSION AZ950028.1 GI:13821255
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE

AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: L column: 19
Seq primer: CACACGAGAAACGCTAGACAC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1.19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0213119"

/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gii4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT 4477
Db 19 TTTT TTTT TTTT TTTT 6

RESULT 1752

LOCUS CF301222 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-P21 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF301222
VERSION CF301222.1 GI:33672983
KEYWORDS EST.

SOURCE

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretioideae; Oryzaceae; Oryza.

1 (bases 1 to 20)

Kim,J.-S., Jun,K.M., Cheong,P.J., Kim,M.-J., Lee,T.H., Shin,Y.C.,
Song,S.-I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of BioScience and Bioinformatics, Yonsei University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

COMMENT

FEATURES

source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultiivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--05-P21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone.lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

0.2%; Score 14; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT 4477
Db 2 TTTT TTTT TTTT TTTT 15

RESULT 1753

LOCUS A2832043/c 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M011211F Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCG2M011211 F, genomic survey sequence.

ACCESSION A2832043
VERSION A2832043.1 GI:13001951
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5605
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 012 row: 1 column: 11
Seq primer: CGTTGTAAACGACGCCAGCT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M011211"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gii4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3276 TTAGAGAGAAAT 3289
 Db 17 TTAGAGAGAAAT 4

RESULT 1754

AZ476017 21 bp DNA linear GSS 04-OCT-2000
 LOCUS
 DEFINITION 1M0294C02R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0294C02 R, genomic survey sequence.

ACCESSION AZ476017
 VERSION AZ476017.1 GI:10634142
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0294 row: C column: 02
 Seq primer: CACACAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0294C02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI:4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4471 TTTT TTTT TTTT TTTT TTTT G 4484
 Db 1 TTTT TTTT TTTT TTTT G 14

RESULT 1755

AZ589400 21 bp DNA linear GSS 13-DEC-2000
 LOCUS
 DEFINITION 1M0398C23F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0398C23 F, genomic survey sequence.

ACCESSION AZ589400
 VERSION AZ589400.1 GI:11711590
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0398 row: C column: 23
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0398C23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI:4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.2%; Score 14; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTTTTTTTTTT 14
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RESULT 1756

Search completed: October 14, 2004, 13:12:42
 Job time : 172 secs

AZ785791

LOCUS 21 bp DNA linear GSS 16-FEB-2001

DEFINITION IM0030019f Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0030019 F, genomic survey sequence.

ACCESSION AZ785791

VERSION AZ785791.1 GI:12922904

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedermauern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

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Insert Length: 10000 Std Error: 0.00

Plate: 0030 row: 0 column: 19

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

location/Qualifiers

1..21

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0030019"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

SOURCE

Query Match 0.2%; Score 14; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTTTTTTTTTT 4477

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 11:35:42 ; Search time 245 Seconds

(without alignments)
3.666 Million cell updates/sec

Title: US-10-007-078-3

Perfect score: 7478
Sequence: 1 actggcagctgcgcggcgccg.....acagtgctctattctta 7478

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 2960 seqs, 60060 residues

Total number of hits satisfying chosen parameters: 5920

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : rn13.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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265	19	0.3	19	1	US-09-227-782-1	Sequence 1, Appl	338	18.4	0.2	21	1	US-09-475-947A-119	Sequence 119, App
266	19	0.3	19	1	US-09-227-782-2	Sequence 2, Appl	339	18.4	0.2	22	1	US-08-123-449A-1	Sequence 1, Appl
267	19	0.3	19	1	US-09-227-782-3	Sequence 3, Appl	340	18.4	0.2	22	1	US-08-123-449A-2	Sequence 2, Appl
268	19	0.3	19	1	US-09-227-782-4	Sequence 4, Appl	341	18.4	0.2	22	1	US-08-458-050-1	Sequence 1, Appl
269	19	0.3	19	1	US-09-227-782-5	Sequence 5, Appl	342	18.4	0.2	22	1	US-08-458-050-2	Sequence 2, Appl
270	19	0.3	19	1	US-09-227-782-6	Sequence 6, Appl	343	18.4	0.2	22	1	US-08-950-196-1	Sequence 1, Appl
271	19	0.3	19	1	US-09-227-782-7	Sequence 7, Appl	344	18.4	0.2	22	1	US-08-950-196-2	Sequence 2, Appl
272	19	0.3	19	1	US-09-227-782-8	Sequence 8, Appl	345	18.2	0.2	19	1	US-08-881-78A-18	Sequence 18, Appl
273	19	0.3	19	1	US-09-227-782-12	Sequence 12, Appl	346	18.2	0.2	19	1	US-09-232-76B-18	Sequence 18, Appl
274	19	0.3	19	1	US-09-227-782-14	Sequence 14, Appl	347	18.2	0.2	23	1	US-08-242-66A-1	Sequence 1, Appl
275	19	0.3	19	1	US-09-227-782-15	Sequence 15, Appl	348	18.2	0.2	23	1	US-08-484-138-1	Sequence 1, Appl
276	19	0.3	19	1	US-09-227-782-25	Sequence 25, Appl	349	18.2	0.2	23	1	PCT-US95-06379-1	Sequence 7, Appl
277	19	0.3	19	1	US-09-619-103-25	Sequence 25, Appl	350	18.2	0.2	24	1	US-09-721-154-7	Sequence 7, Appl
278	19	0.3	19	1	US-09-288-679-1	Sequence 1, Appl	351	18.2	0.2	25	1	US-08-374-144-3	Sequence 3, Appl
279	19	0.3	19	1	US-09-612-531-3	Sequence 3, Appl	352	18.2	0.2	25	1	US-08-775-164-3	Sequence 3, Appl
280	19	0.3	19	1	US-09-612-531-7	Sequence 7, Appl	353	18.2	0.2	25	1	US-08-775-609-3	Sequence 3, Appl
281	19	0.3	19	1	US-09-612-531-13	Sequence 13, Appl	354	18.2	0.2	25	1	US-08-775-609-3	Sequence 3, Appl
282	19	0.3	19	1	US-10-121-135-5	Sequence 5, Appl	355	18.2	0.2	25	1	US-09-866-108A-13907	Sequence 13907, A
283	19	0.3	19	1	US-10-121-135-5	Sequence 5, Appl	356	18.2	0.2	25	1	US-09-866-108A-13910	Sequence 13910, A
284	19	0.3	19	1	US-10-121-135-26	Sequence 26, Appl	357	18.2	0.2	25	1	PCT-US93-06828-3	Sequence 3, Appl
285	19	0.3	19	1	US-09-142-212A-10	Sequence 10, Appl	358	18	0.2	18	1	US-08-621-914A-16	Sequence 16, Appl
286	19	0.3	19	1	US-09-349-040A-3	Sequence 3, Appl	359	18	0.2	18	1	US-08-346-429-3	Sequence 3, Appl
287	19	0.3	19	1	US-09-349-040A-4	Sequence 4, Appl	360	18	0.2	18	1	US-08-358-556A-12	Sequence 12, Appl
288	19	0.3	19	1	US-09-349-040A-5	Sequence 5, Appl	361	18	0.2	18	1	US-08-358-556A-18	Sequence 18, Appl
289	19	0.3	19	1	US-09-409-926-17	Sequence 17, Appl	362	18	0.2	18	1	US-08-469-852A-4	Sequence 4, Appl
290	19	0.3	19	1	US-09-409-926-18	Sequence 18, Appl	363	18	0.2	18	1	US-08-863-539A-17	Sequence 17, Appl
291	19	0.3	19	1	US-10-123-597-1	Sequence 1, Appl	364	18	0.2	18	1	US-08-285-509B-4	Sequence 4, Appl
292	19	0.3	19	1	US-10-123-597-2	Sequence 2, Appl	365	18	0.2	18	1	US-08-884-029-9	Sequence 9, Appl
293	19	0.3	19	1	US-10-123-597-3	Sequence 3, Appl	366	18	0.2	18	1	US-08-941-445A-30	Sequence 30, Appl
294	19	0.3	19	1	US-10-123-597-4	Sequence 4, Appl	367	18	0.2	18	1	US-09-637-751A-6	Sequence 6, Appl
295	19	0.3	19	1	US-10-123-597-5	Sequence 5, Appl	368	18	0.2	18	1	US-09-545-825-9	Sequence 9, Appl
296	19	0.3	19	1	US-10-123-597-6	Sequence 6, Appl	369	18	0.2	18	1	US-09-619-103-24	Sequence 24, Appl
297	19	0.3	19	1	US-10-123-597-7	Sequence 7, Appl	370	18	0.2	18	1	US-09-370-541-14	Sequence 14, Appl
298	19	0.3	19	1	US-10-123-597-8	Sequence 8, Appl	371	18	0.2	18	1	US-10-125-295-9	Sequence 9, Appl
299	19	0.3	19	1	US-10-123-597-12	Sequence 12, Appl	372	18	0.2	18	1	PCT-US94-05407-4	Sequence 4, Appl
300	19	0.3	19	1	US-10-123-597-14	Sequence 14, Appl	373	18	0.2	19	1	US-09-435-806-7	Sequence 7, Appl
301	19	0.3	19	1	US-10-123-597-15	Sequence 15, Appl	374	18	0.2	26	1	US-08-487-41B-42	Sequence 42, Appl
302	19	0.3	19	1	US-10-123-597-25	Sequence 25, Appl	375	18	0.2	26	1	US-08-927-561-42	Sequence 42, Appl
303	19	0.3	19	1	US-09-349-033A-1	Sequence 1, Appl	376	18	0.2	26	1	PCT-US96-05388-42	Sequence 42, Appl
304	19	0.3	19	1	US-09-435-806-6	Sequence 6, Appl	377	18	0.2	27	1	US-08-946-914-50	Sequence 50, Appl
305	19	0.3	20	1	US-08-482-918-12	Sequence 32, Appl	378	18	0.2	27	1	US-08-584-040-1083	Sequence 1083, Ap
306	19	0.3	20	1	US-09-224-681-32	Sequence 32, Appl	379	18	0.2	27	1	US-08-584-040-7130	Sequence 7130, Ap
307	19	0.3	20	1	US-08-336-728A-32	Sequence 32, Appl	380	18	0.2	27	1	US-09-656-450-50	Sequence 50, Appl
308	19	0.3	21	1	US-08-359-295C-23	Sequence 23, Appl	381	17.8	0.2	21	1	US-09-422-878-9116	Sequence 9116, Ap
309	19	0.3	21	1	US-08-485-105A-23	Sequence 23, Appl	382	17.8	0.2	23	1	US-08-621-914A-6	Sequence 6, Appl
310	19	0.3	21	1	US-09-183-650-23	Sequence 23, Appl	383	17.8	0.2	23	1	US-09-056-052-9	Sequence 9, Appl
311	19	0.3	23	1	PCT-US94-05407-7	Sequence 7, Appl	384	17.8	0.2	24	1	US-08-938-830-60	Sequence 60, Appl
312	19	0.3	23	1	PCT-US94-05407-8	Sequence 8, Appl	385	17.8	0.2	24	1	US-09-688-990-2	Sequence 2, Appl
313	19	0.3	26	1	US-08-623-354-8	Sequence 8, Appl	386	17.8	0.2	25	1	US-08-811-692-41	Sequence 41, Appl
314	19	0.3	28	1	US-08-762-106-11	Sequence 11, Appl	387	17.8	0.2	25	1	US-09-866-108A-13911	Sequence 13911, A
315	19	0.3	28	1	US-09-320-774-11	Sequence 11, Appl	388	17.8	0.2	25	1	US-08-336-728A-34	Sequence 34, Appl
316	19	0.3	29	1	US-09-304-232-664	Sequence 464, Appl	389	17.8	0.2	25	1	PCT-US96-10545A-41	Sequence 41, Appl
317	18.8	0.3	23	1	US-08-018-129-15	Sequence 15, Appl	390	17.6	0.2	24	1	US-08-942-112B-5	Sequence 5, Appl
318	18.8	0.3	23	1	US-08-448-250-15	Sequence 15, Appl	391	17.6	0.2	25	1	US-09-596-120-18	Sequence 18, Appl
319	18.8	0.3	23	1	US-09-283-257-15	Sequence 15, Appl	392	17.6	0.2	25	1	US-09-596-120-19	Sequence 19, Appl
320	18.8	0.3	25	1	US-08-115-497-1	Sequence 1, Appl	393	17.6	0.2	26	1	US-07-885-570A-1	Sequence 1, Appl
321	18.8	0.3	25	1	US-08-466-670-1	Sequence 1, Appl	394	17.6	0.2	26	1	US-08-298-887A-1	Sequence 1, Appl
322	18.8	0.3	26	1	US-08-014-943A-21	Sequence 21, Appl	395	17.6	0.2	26	1	US-08-241-943-1	Sequence 1, Appl
323	18.8	0.3	26	1	US-08-486-421-15	Sequence 15, Appl	396	17.6	0.2	26	1	US-08-378-88B-1	Sequence 1, Appl
324	18.8	0.3	26	1	US-08-470-911-15	Sequence 15, Appl	397	17.6	0.2	26	1	US-08-298-829-1	Sequence 1, Appl
325	18.8	0.3	26	1	US-08-486-809-15	Sequence 15, Appl	398	17.6	0.2	26	1	US-08-811-094-1	Sequence 1, Appl

399	17.6	0.2	26	1	US-08-467-504-10	Sequence 10, Appl	472	16.8	0.2	22	1	US-09-056-285A-30	Sequence 30, Appl
400	17.6	0.2	26	1	US-09-679-263-13	Sequence 13, Appl	473	16.8	0.2	23	1	US-08-068-945A-25	Sequence 25, Appl
401	17.6	0.2	26	1	PCT-US94-11121-1	Sequence 1, Appl	C 474	16.8	0.2	23	1	US-08-442-806-25	Sequence 25, Appl
402	17.6	0.2	27	1	US-08-985-162-999	Sequence 999, App	475	16.8	0.2	25	1	US-08-161-281A-10	Sequence 10, Appl
403	17.6	0.2	27	1	US-09-126-280-17	Sequence 17, App	476	16.8	0.2	25	1	US-08-648-709-4	Sequence 4, Appl
404	17.6	0.2	27	1	US-08-584-040-310	Sequence 310, App	C 477	16.8	0.2	25	1	US-09-010-641-34	Sequence 34, Appl
C 405	17.6	0.2	27	1	US-08-584-040-3684	Sequence 3684, Ap	C 478	16.8	0.2	25	1	US-09-356-281-34	Sequence 34, Appl
C 406	17.6	0.2	27	1	US-09-401-063-999	Sequence 999, App	479	16.8	0.2	25	1	US-09-393-389-4	Sequence 4, Appl
C 407	17.6	0.2	40	1	US-09-306-290-25	Sequence 25, App	480	16.8	0.2	25	1	US-08-866-108A-13913	Sequence 13913, A
408	17.4	0.2	19	1	US-08-410-540-5	Sequence 5, Appl	481	16.8	0.2	30	1	US-08-433-505-9	Sequence 9, Appl
409	17.4	0.2	20	1	US-07-912-900-20	Sequence 20, Appl	482	16.8	0.2	30	1	US-08-870-730-9	Sequence 9, Appl
410	17.4	0.2	20	1	US-08-285-309-20	Sequence 20, Appl	C 483	16.8	0.2	30	1	US-09-083-123-3	Sequence 3, Appl
411	17.4	0.2	20	1	US-08-313-075A-11	Sequence 11, Appl	C 484	16.8	0.2	30	1	US-09-083-123-7	Sequence 7, Appl
412	17.4	0.2	20	1	US-08-502-046-20	Sequence 20, Appl	485	16.8	0.2	30	1	US-08-882-649A-10	Sequence 10, Appl
413	17.4	0.2	20	1	US-08-927-219-56	Sequence 56, Appl	C 486	16.6	0.2	23	1	US-09-686-597-26	Sequence 26, Appl
414	17.4	0.2	23	1	US-08-621-914A-5	Sequence 5, Appl	C 487	16.6	0.2	23	1	US-09-083-266-11	Sequence 11, Appl
C 415	17.4	0.2	23	1	US-09-056-052-8	Sequence 8, Appl	C 488	16.6	0.2	24	1	US-08-529-190B-22	Sequence 22, Appl
C 416	17.4	0.2	27	1	US-09-475-947A-153	Sequence 153, App	489	16.6	0.2	24	1	US-08-863-639A-27	Sequence 27, Appl
C 417	17.4	0.2	35	1	US-08-173-489C-20	Sequence 20, Appl	490	16.6	0.2	24	1	US-09-157-210-4	Sequence 4, Appl
C 418	17.2	0.2	19	1	US-09-130-079-1	Sequence 1, Appl	491	16.6	0.2	24	1	US-09-581-493-9	Sequence 9, Appl
C 419	17.2	0.2	22	1	US-09-078-871A-3	Sequence 3, Appl	C 492	16.6	0.2	25	1	US-09-651-011A-5	Sequence 5, Appl
C 420	17.2	0.2	22	1	US-09-629-222A-7	Sequence 7, Appl	C 493	16.6	0.2	25	1	US-08-484-557C-12	Sequence 12, Appl
421	17.2	0.2	23	1	US-08-621-914A-4	Sequence 4, Appl	C 494	16.6	0.2	25	1	US-08-487-426B-12	Sequence 12, Appl
C 422	17.2	0.2	23	1	US-07-869-933-7	Sequence 7, Appl	C 495	16.6	0.2	25	1	US-08-487-720A-12	Sequence 12, Appl
C 423	17.2	0.2	23	1	US-09-056-052-7	Sequence 7, Appl	496	16.6	0.2	25	1	US-09-528-760A-10	Sequence 10, Appl
C 424	17.2	0.2	23	1	US-09-103-663-7	Sequence 7, Appl	497	16.6	0.2	25	1	US-09-951-843-10	Sequence 10, Appl
C 425	17.2	0.2	23	1	US-09-632-098-24	Sequence 24, Appl	C 498	16.6	0.2	25	1	US-09-866-108A-3233	Sequence 3233, Ap
426	17.2	0.2	24	1	US-08-356-790-9	Sequence 9, Appl	C 499	16.6	0.2	25	1	US-09-866-108A-3234	Sequence 3234, Ap
C 427	17.2	0.2	24	1	US-09-360-545-100	Sequence 100, App	C 500	16.6	0.2	25	1	US-09-866-108A-3335	Sequence 3235, Ap
428	17.2	0.2	24	1	US-09-360-545-101	Sequence 101, App	C 501	16.6	0.2	25	1	US-09-866-108A-4407	Sequence 4407, Ap
C 429	17.2	0.2	24	1	US-09-496-632C-11	Sequence 11, Appl	C 502	16.6	0.2	25	1	US-09-866-108A-4408	Sequence 4408, Ap
430	17.2	0.2	24	1	US-09-496-632C-12	Sequence 12, Appl	C 503	16.6	0.2	25	1	US-09-866-108A-4409	Sequence 4409, Ap
431	17.2	0.2	25	1	US-09-389-642A-11	Sequence 11, Appl	504	16.6	0.2	25	1	US-09-866-108A-5201	Sequence 5201, Ap
432	17.2	0.2	25	1	US-09-899-642A-11	Sequence 11, Appl	505	16.6	0.2	25	1	US-09-866-108A-5202	Sequence 5202, Ap
433	17.2	0.2	25	1	US-09-866-108A-113906	Sequence 13906, A	506	16.6	0.2	25	1	US-09-866-108A-5203	Sequence 5203, Ap
434	17.2	0.2	26	1	US-08-632-575B-7	Sequence 7, Appl	507	16.6	0.2	25	1	US-09-866-108A-12694	Sequence 12694, A
435	17.2	0.2	26	1	US-08-747-536-17	Sequence 17, Appl	508	16.6	0.2	32	1	US-09-866-108A-12695	Sequence 12695, A
436	17.2	0.2	26	1	US-09-199-542B-7	Sequence 7, Appl	509	16.6	0.2	32	1	US-10-003-998A-4	Sequence 4, Appl
C 437	17.2	0.2	30	1	US-09-725-265-11	Sequence 11, Appl	C 510	16.4	0.2	18	1	US-08-679-645-1167	Sequence 1167, Ap
C 438	17.2	0.2	30	1	US-09-725-265-13	Sequence 13, Appl	511	16.4	0.2	19	1	US-09-205-995-48	Sequence 48, Appl
C 439	17.2	0.2	33	1	US-09-061-026-26	Sequence 26, Appl	512	16.4	0.2	19	1	US-09-422-927-10119	Sequence 10119, A
C 440	17.2	0.2	33	1	US-09-466-138-26	Sequence 26, Appl	513	16.4	0.2	20	1	US-08-775-951-49	Sequence 8, Appl
441	17	0.2	17	1	US-08-851-843A-132	Sequence 132, App	C 514	16.4	0.2	21	1	US-08-941-100-3	Sequence 3, Appl
442	17	0.2	17	1	US-09-250-075-5	Sequence 5, Appl	C 515	16.4	0.2	21	1	US-08-941-100-8	Sequence 8, Appl
443	17	0.2	17	1	US-08-854-050-132	Sequence 132, App	516	16.4	0.2	23	1	US-09-161-466-19	Sequence 19, Appl
444	17	0.2	17	1	US-09-430-323-132	Sequence 132, App	C 517	16.4	0.2	24	1	US-09-360-416-74	Sequence 14, Appl
445	17	0.2	17	1	US-08-584-040-2549	Sequence 2549, Ap	C 518	16.4	0.2	25	1	US-08-367-101-140	Sequence 140, App
446	17	0.2	17	1	US-08-584-040-2550	Sequence 2550, Ap	C 519	16.4	0.2	25	1	US-08-592-541-140	Sequence 140, App
C 447	17	0.2	17	1	US-09-619-103-23	Sequence 23, Appl	C 520	16.4	0.2	25	1	US-09-124-698-140	Sequence 140, App
448	17	0.2	17	1	US-09-726-096A-5	Sequence 5, Appl	C 521	16.4	0.2	25	1	US-09-127-480-140	Sequence 140, App
449	17	0.2	17	1	US-09-371-772B-1073	Sequence 1073, Ap	C 522	16.4	0.2	25	1	US-08-496-841C-140	Sequence 140, App
450	17	0.2	17	1	US-09-371-772B-1074	Sequence 1074, Ap	C 523	16.4	0.2	25	1	US-09-124-523-140	Sequence 140, App
451	17	0.2	18	1	US-09-637-751A-5	Sequence 5, Appl	C 524	16.4	0.2	25	1	US-09-636-796A-140	Sequence 140, App
452	17	0.2	19	1	US-08-973-857-6	Sequence 6, Appl	C 525	16.2	0.2	21	1	US-08-294-424-27	Sequence 27, Appl
C 453	17	0.2	20	1	US-09-198-452A-3717	Sequence 3717, Ap	526	16.2	0.2	21	1	US-08-472-651-20	Sequence 20, Appl
454	17	0.2	21	1	US-08-704-966-7	Sequence 7, Appl	527	16.2	0.2	21	1	US-08-474-661-20	Sequence 20, Appl
455	17	0.2	21	1	US-08-705-438-7	Sequence 7, Appl	528	16.2	0.2	21	1	US-08-611-977-20	Sequence 20, Appl
456	17	0.2	25	1	US-09-866-108A-5298	Sequence 5298, Ap	C 529	16.2	0.2	21	1	US-08-863-639A-52	Sequence 52, Appl
457	17	0.2	25	1	US-09-866-108A-5299	Sequence 5299, Ap	C 530	16.2	0.2	21	1	US-08-863-639A-55	Sequence 55, Appl
458	17	0.2	25	1	US-09-866-108A-12696	Sequence 12696, A	531	16.2	0.2	21	1	US-08-863-639A-67	Sequence 67, Appl
459	17	0.2	25	1	US-09-866-108A-12697	Sequence 12697, A	C 532	16.2	0.2	21	1	US-08-863-639A-68	Sequence 68, Appl
C 460	17	0.2	25	1	US-09-866-108A-13467	Sequence 13467, A	533	16.2	0.2	21	1	US-08-863-639A-71	Sequence 71, Appl
461	17	0.2	26	1	US-08-291-011-10	Sequence 10, Appl	534	16.2	0.2	21	1	US-08-416-214A-11	Sequence 11, Appl
462	17	0.2	26	1	US-09-282-147-1	Sequence 1, Appl	535	16.2	0.2	21	1	US-09-328-942-8	Sequence 8, Appl
463	17	0.2	26	1	US-09-266-065-10	Sequence 10, Appl	536	16.2	0.2	21	1	US-09-422-978-11535	Sequence 11535, A
C 464	17	0.2	26	1	US-09-538-709-415	Sequence 415, Appl	537	16.2	0.2	21	1	US-08-390-850-7	Sequence 7, Appl
465	17	0.2	26	1	US-09-935-247-10	Sequence 10, Appl	C 538	16.2	0.2	22	1	US-08-435-634-7	Sequence 7, Appl
C 466	17	0.2	30	1	US-09-725-265-10	Sequence 10, Appl	C 539	16.2	0.2	22	1	US-09-009-913-156	Sequence 156, App
C 467	17	0.2	30	1	US-09-725-265-12	Sequence 12, Appl	C 540	16.2	0.2	22	1	US-09-230-222-16	Sequence 23, Appl
C 468	17	0.2	31	1	US-09-268-505B-13	Sequence 13, Appl	541	16.2	0.2	23	1	US-09-230-222B-23	Sequence 23, Appl
C 469	16.8	0.2	20	1	US-08-568-271-1	Sequence 1, Appl	542	16.2	0.2	23	1	US-09-686-597-24	Sequence 24, Appl
470	16.8	0.2	20	1	US-09-661-753-35	Sequence 35, Appl	C 543	16.2	0.2	23	1	US-09-686-597-25	Sequence 25, Appl
471	16.8	0.2	20	1	US-09-723-368-5	Sequence 5, Appl	C 544	16.2	0.2	23	1	US-09-686-597-25	Sequence 25, Appl

C 545	16.2	0.2	23	1	US-09-686-597-27	Sequence 27, Appl	C 618	15.8	0.2	20	1	US-09-357-070-22	Sequence 22, Appl
C 546	16.2	0.2	24	1	US-08-465-590-94	Sequence 94, Appl	C 619	15.8	0.2	20	1	US-09-287-796-14	Sequence 14, Appl
C 547	16.2	0.2	24	1	US-08-570-155-16	Sequence 16, Appl	C 620	15.8	0.2	20	1	US-09-444-053-26	Sequence 26, Appl
C 548	16.2	0.2	24	1	US-08-487-799-17	Sequence 17, Appl	C 621	15.8	0.2	20	1	US-09-030-701-65	Sequence 65, Appl
C 549	16.2	0.2	24	1	US-09-030-701-29	Sequence 29, Appl	C 622	15.8	0.2	20	1	US-09-130-616-14	Sequence 14, Appl
C 550	16.2	0.2	24	1	US-09-286-098-61	Sequence 61, Appl	C 623	15.8	0.2	20	1	US-09-657-042A-39	Sequence 39, Appl
C 551	16.2	0.2	24	1	US-08-711-417C-94	Sequence 94, Appl	C 624	15.8	0.2	20	1	US-09-082-649B-57	Sequence 57, Appl
C 552	16.2	0.2	24	1	US-08-960-774-61	Sequence 61, Appl	C 625	15.8	0.2	20	1	US-09-232-146-59	Sequence 59, Appl
C 553	16.2	0.2	24	1	US-09-296-280-48	Sequence 48, Appl	C 626	15.8	0.2	20	1	US-09-732-199A-54	Sequence 54, Appl
C 554	16.2	0.2	24	1	US-09-325-193A-52	Sequence 52, Appl	C 627	15.8	0.2	20	1	US-08-108-591B-5	Sequence 5, Appl
C 555	16.2	0.2	24	1	US-09-191-170-55	Sequence 55, Appl	C 628	15.8	0.2	20	1	US-09-535-008-11	Sequence 11, Appl
C 556	16.2	0.2	24	1	US-09-723-909-94	Sequence 94, Appl	C 629	15.8	0.2	20	1	US-09-690-364-59	Sequence 99, Appl
C 557	16.2	0.2	24	1	US-09-337-619-61	Sequence 61, Appl	C 630	15.8	0.2	20	1	US-09-725-265-35	Sequence 35, Appl
C 558	16.2	0.2	24	1	PCT-US93-08743-94	Sequence 94, Appl	C 631	15.8	0.2	21	1	US-09-432-978-7625	Sequence 7625, Ap
C 559	16.2	0.2	25	1	US-08-115-497-1	Sequence 1, Appl	C 632	15.8	0.2	21	1	US-09-422-978-9563	Sequence 9563, Ap
C 560	16.2	0.2	25	1	US-08-466-670-1	Sequence 1, Appl	C 633	15.8	0.2	21	1	US-09-422-978-10315	Sequence 10315, A
C 561	16	0.2	16	1	US-08-087-387-6	Sequence 6, Appl	C 634	15.8	0.2	22	1	US-08-546-130A-23	Sequence 23, Appl
C 562	16	0.2	16	1	US-08-455-627-6	Sequence 6, Appl	C 635	15.8	0.2	22	1	US-08-680-395-11	Sequence 31, Appl
C 563	16	0.2	16	1	US-07-971-978-36	Sequence 36, Appl	C 636	15.8	0.2	22	1	US-08-291-011-9	Sequence 9, Appl
C 564	16	0.2	16	1	US-07-971-978-42	Sequence 42, Appl	C 637	15.8	0.2	22	1	US-09-066-641-12	Sequence 12, Appl
C 565	16	0.2	16	1	US-07-971-978-60	Sequence 60, Appl	C 638	15.8	0.2	22	1	US-09-266-065-9	Sequence 9, Appl
C 566	16	0.2	16	1	US-08-461-271-6	Sequence 6, Appl	C 639	15.8	0.2	22	1	US-09-935-247-9	Sequence 9, Appl
C 567	16	0.2	16	1	US-08-415-370-2	Sequence 2, Appl	C 640	15.8	0.2	23	1	US-09-262-773-203	Sequence 203, App
C 568	16	0.2	16	1	US-08-713-685A-6	Sequence 6, Appl	C 641	15.8	0.2	23	1	US-08-934-386-30	Sequence 30, Appl
C 569	16	0.2	16	1	US-08-689-856-6	Sequence 6, Appl	C 642	15.8	0.2	23	1	US-10-238-483-1	Sequence 1, Appl
C 570	16	0.2	16	1	US-08-687-551-15	Sequence 15, Appl	C 643	15.8	0.2	24	1	US-08-520-928-3	Sequence 3, Appl
C 571	16	0.2	16	1	US-09-070-477-6	Sequence 6, Appl	C 644	15.8	0.2	24	1	US-08-570-155-17	Sequence 17, Appl
C 572	16	0.2	16	1	US-09-141-764-2	Sequence 2, Appl	C 645	15.8	0.2	24	1	US-09-004-113-23	Sequence 23, Appl
C 573	16	0.2	16	1	US-08-851-843A-131	Sequence 131, App	C 646	15.8	0.2	24	1	US-08-974-549A-472	Sequence 472, App
C 574	16	0.2	16	1	US-08-854-050-131	Sequence 131, App	C 647	15.8	0.2	24	1	US-08-912-951-339	Sequence 339, App
C 575	16	0.2	16	1	US-09-430-323-131	Sequence 131, App	C 648	15.8	0.2	24	1	US-09-402-181B-472	Sequence 472, App
C 576	16	0.2	16	1	US-09-507-345A-2	Sequence 2, Appl	C 649	15.8	0.2	24	1	US-09-721-456-472	Sequence 472, App
C 577	16	0.2	16	1	US-09-619-103-22	Sequence 22, Appl	C 650	15.8	0.2	24	1	US-08-208-486-79	Sequence 79, Appl
C 578	16	0.2	16	1	US-09-739-928-2	Sequence 2, Appl	C 651	15.8	0.2	29	1	US-09-244-794A-8	Sequence 8, Appl
C 579	16	0.2	17	1	US-08-821-827C-30	Sequence 30, Appl	C 652	15.8	0.2	29	1	US-09-007-005-8	Sequence 8, Appl
C 580	16	0.2	17	1	US-09-290-202B-30	Sequence 30, Appl	C 653	15.8	0.2	29	1	US-09-247-190-8	Sequence 8, Appl
C 581	16	0.2	17	1	US-08-584-040-2548	Sequence 2548, Ap	C 654	15.8	0.2	29	1	US-09-244-796-8	Sequence 8, Appl
C 582	16	0.2	17	1	US-08-584-040-2551	Sequence 2551, Ap	C 655	15.8	0.2	29	1	US-09-238-710-8	Sequence 8, Appl
C 583	16	0.2	17	1	US-09-788-338-3	Sequence 3, Appl	C 656	15.8	0.2	29	1	US-09-282-734-4	Sequence 3, Appl
C 584	16	0.2	17	1	US-09-300-958A-64	Sequence 64, Appl	C 657	15.8	0.2	29	1	US-08-400-375-13	Sequence 13, Appl
C 585	16	0.2	17	1	US-09-371-772B-1072	Sequence 1072, Ap	C 658	15.8	0.2	29	1	US-08-910-632-6	Sequence 6, Appl
C 586	16	0.2	17	1	US-09-371-772B-1075	Sequence 1075, Ap	C 659	15.8	0.2	29	1	US-08-805-631A-6	Sequence 6, Appl
C 587	16	0.2	18	1	US-08-927-274A-6	Sequence 6, Appl	C 660	15.8	0.2	29	1	US-09-569-344-6	Sequence 6, Appl
C 588	16	0.2	18	1	US-09-637-751A-7	Sequence 7, Appl	C 661	15.8	0.2	30	1	US-09-648-040-4	Sequence 4, Appl
C 589	16	0.2	18	1	US-09-422-978-4670	Sequence 4670, Ap	C 662	15.8	0.2	30	1	US-09-725-265-9	Sequence 9, Appl
C 590	16	0.2	20	1	US-08-650-598-8	Sequence 8, Appl	C 663	15.8	0.2	32	1	US-09-750-401-10	Sequence 10, Appl
C 591	16	0.2	20	1	US-09-228-942-7	Sequence 7, Appl	C 664	15.8	0.2	33	1	5478746-1	Patent No. 5478746
C 592	16	0.2	20	1	US-09-965-599-4	Sequence 4, Appl	C 665	15.6	0.2	22	1	US-08-937-067-17	Sequence 17, Appl
C 593	16	0.2	20	1	US-09-198-452A-4311	Sequence 4311, Ap	C 666	15.6	0.2	22	1	US-08-056-200-35	Sequence 35, Appl
C 594	16	0.2	22	1	US-08-318-837-37	Sequence 37, Appl	C 667	15.6	0.2	22	1	US-08-056-200-39	Sequence 39, Appl
C 595	16	0.2	24	1	US-08-863-639A-27	Sequence 27, Appl	C 668	15.6	0.2	22	1	US-08-410-540-20	Sequence 20, Appl
C 596	16	0.2	24	1	US-08-200-807-3	Sequence 3, Appl	C 669	15.6	0.2	22	1	US-08-459-899-1	Sequence 1, Appl
C 597	16	0.2	24	1	US-08-242-402-13	Sequence 13, Appl	C 670	15.6	0.2	22	1	US-08-800-644-35	Sequence 35, Appl
C 598	16	0.2	24	1	US-08-488-305A-3	Sequence 3, Appl	C 671	15.6	0.2	22	1	US-08-800-644-35	Sequence 35, Appl
C 599	16	0.2	24	1	US-08-808-474A-9	Sequence 9, Appl	C 672	15.6	0.2	22	1	US-08-964-143-1	Sequence 1, Appl
C 600	16	0.2	24	1	US-08-808-474A-10	Sequence 10, Appl	C 673	15.6	0.2	22	1	US-09-344-667-43	Sequence 43, Appl
C 601	16	0.2	24	1	US-08-682-423-26	Sequence 26, Appl	C 674	15.6	0.2	22	1	US-09-344-667-46	Sequence 46, Appl
C 602	16	0.2	24	1	US-09-142-521-6	Sequence 6, Appl	C 675	15.6	0.2	22	1	US-09-693-352-43	Sequence 43, Appl
C 603	16	0.2	24	1	US-09-235-614-10	Sequence 10, Appl	C 676	15.6	0.2	22	1	US-09-693-352-46	Sequence 46, Appl
C 604	16	0.2	24	1	US-09-235-614-11	Sequence 11, Appl	C 677	15.6	0.2	22	1	US-09-693-352A-43	Sequence 43, Appl
C 605	16	0.2	24	1	US-09-018-584A-92	Sequence 92, Appl	C 678	15.6	0.2	22	1	US-09-693-005A-46	Sequence 46, Appl
C 606	16	0.2	24	1	US-09-298-886-6	Sequence 6, Appl	C 679	15.6	0.2	22	1	US-09-603-830-43	Sequence 43, Appl
C 607	16	0.2	24	1	US-09-006-755B-10	Sequence 10, Appl	C 680	15.6	0.2	22	1	US-09-603-830-46	Sequence 46, Appl
C 608	16	0.2	24	1	US-09-356-806-82	Sequence 82, Appl	C 681	15.6	0.2	22	1	US-09-976-910-4	Sequence 4, Appl
C 609	16	0.2	24	1	US-09-999-672-6	Sequence 6, Appl	C 682	15.6	0.2	22	1	US-09-976-978A-46	Sequence 46, Appl
C 610	16	0.2	24	1	PCT-US93-08329-4	Sequence 4, Appl	C 683	15.6	0.2	22	1	US-09-976-978A-46	Sequence 46, Appl
C 611	16	0.2	24	1	PCT-US95-05141-26	Sequence 26, Appl	C 684	15.6	0.2	22	1	US-09-961-949A-43	Sequence 43, Appl
C 612	15.8	0.2	19	1	US-09-422-978-5276	Sequence 5276, Ap	C 685	15.6	0.2	22	1	US-09-961-949A-46	Sequence 46, Appl
C 613	15.8	0.2	20	1	US-08-117-952-613	Sequence 613, App	C 686	15.6	0.2	22	1	US-09-966-919A-43	Sequence 43, Appl
C 614	15.8	0.2	20	1	US-08-173-489C-18	Sequence 18, Appl	C 687	15.6	0.2	22	1	US-09-966-919A-46	Sequence 46, Appl
C 615	15.8	0.2	20	1	US-08-910-629A-14	Sequence 14, Appl	C 688	15.6	0.2	22	1	US-09-611-627-49	Sequence 49, Appl
C 616	15.8	0.2	20	1	US-08-507-032-8	Sequence 8, Appl	C 689	15.6	0.2	22	1	US-09-957-113A-43	Sequence 43, Appl
C 617	15.8	0.2	20	1	US-08-914-961-2	Sequence 2, Appl	C 690	15.6	0.2	22	1	US-09-957-113A-46	Sequence 46, Appl

C 691	15.6	0.2	22	1	US-09-966-312-43	Sequence 43, Appl	C 764	15.4	0.2	19	1	US-09-814-986-39	Sequence 39, Appl
C 692	15.6	0.2	22	1	US-09-966-312-46	Sequence 46, Appl	C 765	15.4	0.2	19	1	US-09-530-098B-26	Sequence 26, Appl
C 693	15.6	0.2	22	1	US-09-975-062A-43	Sequence 43, Appl	C 766	15.4	0.2	20	1	US-08-715-461-5	Sequence 5, Appl
C 694	15.6	0.2	22	1	US-09-975-062A-46	Sequence 46, Appl	C 767	15.4	0.2	20	1	US-09-517-584A-13	Sequence 13, Appl
C 695	15.6	0.2	22	1	US-09-976-971A-43	Sequence 43, Appl	C 768	15.4	0.2	20	1	US-09-021-701-728	Sequence 728, App
C 696	15.6	0.2	22	1	US-09-976-971A-46	Sequence 46, Appl	C 769	15.4	0.2	20	1	US-09-021-701-729	Sequence 729, App
C 697	15.6	0.2	23	1	US-08-025-038-2	Sequence 2, Appl	C 770	15.4	0.2	20	1	US-09-021-701-730	Sequence 730, App
C 698	15.6	0.2	23	1	US-08-484-557C-13	Sequence 13, Appl	C 771	15.4	0.2	20	1	US-09-021-701-731	Sequence 731, App
C 699	15.6	0.2	23	1	US-08-487-426B-13	Sequence 13, Appl	C 772	15.4	0.2	20	1	US-09-844-63A-46	Sequence 46, Appl
C 700	15.6	0.2	23	1	US-08-659-605A-19	Sequence 19, Appl	C 773	15.4	0.2	20	1	US-09-792-59A-20	Sequence 20, Appl
C 701	15.6	0.2	23	1	US-08-450-945-52	Sequence 52, Appl	C 774	15.4	0.2	20	1	US-09-907-843-23	Sequence 23, Appl
C 702	15.6	0.2	23	1	US-08-487-720A-13	Sequence 13, Appl	C 775	15.4	0.2	20	1	US-09-470-443-17	Sequence 17, Appl
C 703	15.6	0.2	23	1	US-08-637-115-3	Sequence 3, Appl	C 776	15.4	0.2	20	1	US-09-300-008B-19	Sequence 39, Appl
C 704	15.6	0.2	23	1	US-08-976-161-52	Sequence 52, Appl	C 777	15.4	0.2	20	1	US-09-844-525A-79	Sequence 6348, Ap
C 705	15.6	0.2	23	1	US-09-338-907-461	Sequence 461, App	C 778	15.4	0.2	20	1	US-09-422-978-6348	Sequence 22, Appl
C 706	15.6	0.2	23	1	US-09-282-147-30	Sequence 30, Appl	C 779	15.4	0.2	20	1	US-09-601-144-22	Sequence 22, Appl
C 707	15.6	0.2	23	1	US-09-218-207-461	Sequence 461, App	C 780	15.4	0.2	20	1	US-09-903-413-8	Sequence 8, Appl
C 708	15.6	0.2	23	1	US-09-395-604A-3	Sequence 3, Appl	C 781	15.4	0.2	21	1	US-09-665-615B-177	Sequence 177, App
C 709	15.6	0.2	23	1	US-08-650-965-4	Sequence 4, Appl	C 782	15.4	0.2	21	1	US-08-413-813-43	Sequence 43, Appl
C 710	15.6	0.2	23	1	US-09-687-910-3	Sequence 3, Appl	C 783	15.4	0.2	21	1	US-08-467-346-43	Sequence 43, Appl
C 711	15.6	0.2	24	1	US-08-014-943A-11	Sequence 11, Appl	C 784	15.4	0.2	21	1	US-08-628-540-9	Sequence 9, Appl
C 712	15.6	0.2	24	1	US-08-486-421-46	Sequence 46, Appl	C 785	15.4	0.2	21	1	US-08-941-100-4	Sequence 4, Appl
C 713	15.6	0.2	24	1	US-08-411-796-187	Sequence 187, App	C 786	15.4	0.2	21	1	US-09-422-978-9992	Sequence 9992, Ap
C 714	15.6	0.2	24	1	US-08-470-911-46	Sequence 46, Appl	C 787	15.4	0.2	21	1	US-09-422-978-11139	Sequence 11139, A
C 715	15.6	0.2	24	1	US-08-662-335A-1	Sequence 1, Appl	C 788	15.4	0.2	21	1	US-09-536-393-23	Sequence 23, Appl
C 716	15.6	0.2	24	1	US-08-808-474A-8	Sequence 8, Appl	C 789	15.4	0.2	21	1	US-09-536-393-29	Sequence 29, Appl
C 717	15.6	0.2	24	1	US-08-808-474A-11	Sequence 11, Appl	C 790	15.4	0.2	22	1	US-08-457-272B-18	Sequence 18, Appl
C 718	15.6	0.2	24	1	US-08-486-809-46	Sequence 46, Appl	C 791	15.4	0.2	22	1	US-08-761-704-5	Sequence 5, Appl
C 719	15.6	0.2	24	1	US-08-859-998-893	Sequence 893, App	C 792	15.4	0.2	22	1	US-08-722-240-2	Sequence 2, Appl
C 720	15.6	0.2	24	1	US-08-924-695A-22	Sequence 22, Appl	C 793	15.4	0.2	22	1	US-09-095-372-5	Sequence 5, Appl
C 721	15.6	0.2	24	1	US-08-471-039-187	Sequence 187, App	C 794	15.4	0.2	23	1	US-08-182-172-16	Sequence 16, Appl
C 722	15.6	0.2	24	1	US-08-624-290B-9	Sequence 9, Appl	C 795	15.4	0.2	23	1	US-09-870-956-41	Sequence 41, Appl
C 723	15.6	0.2	24	1	US-09-235-614-8	Sequence 8, Appl	C 796	15.4	0.2	27	1	US-09-325-55A-18	Sequence 18, Appl
C 724	15.6	0.2	24	1	US-09-235-614-9	Sequence 9, Appl	C 797	15.4	0.2	30	1	US-09-723-265-8	Sequence 8, Appl
C 725	15.6	0.2	24	1	US-09-463-702A-8	Sequence 8, Appl	C 798	15.4	0.2	32	1	US-09-619-103-14	Sequence 14, Appl
C 726	15.6	0.2	24	1	US-09-225-928-893	Sequence 893, App	C 799	15.2	0.2	17	1	US-09-390-324B-2	Sequence 2, Appl
C 727	15.6	0.2	24	1	US-09-487-130-1	Sequence 1, Appl	C 800	15.2	0.2	17	1	US-10-015-593-2	Sequence 2, Appl
C 728	15.6	0.2	24	1	US-09-487-130-2	Sequence 2, Appl	C 801	15.2	0.2	20	1	US-08-031-143B-12	Sequence 12, Appl
C 729	15.6	0.2	24	1	US-09-487-130-3	Sequence 3, Appl	C 802	15.2	0.2	20	1	US-08-564-002-11	Sequence 11, Appl
C 730	15.6	0.2	24	1	US-09-487-130-4	Sequence 4, Appl	C 803	15.2	0.2	20	1	US-08-890-980-61	Sequence 61, Appl
C 731	15.6	0.2	24	1	US-09-487-130-5	Sequence 5, Appl	C 804	15.2	0.2	20	1	US-09-226-568-37	Sequence 37, Appl
C 732	15.6	0.2	24	1	US-09-487-130-6	Sequence 6, Appl	C 805	15.2	0.2	20	1	US-08-890-979-61	Sequence 61, Appl
C 733	15.6	0.2	24	1	US-09-641-318-22	Sequence 22, Appl	C 806	15.2	0.2	20	1	US-09-289-267-56	Sequence 56, Appl
C 734	15.6	0.2	24	1	US-08-985-492-24	Sequence 24, Appl	C 807	15.2	0.2	20	1	US-09-032-894-61	Sequence 61, Appl
C 735	15.6	0.2	24	1	US-09-699-135-8	Sequence 8, Appl	C 808	15.2	0.2	20	1	US-08-765-340-10	Sequence 10, Appl
C 736	15.6	0.2	24	1	US-08-559-390-187	Sequence 187, App	C 809	15.2	0.2	20	1	US-09-407-675-2	Sequence 2, Appl
C 737	15.6	0.2	24	1	US-09-225-201B-893	Sequence 893, App	C 810	15.2	0.2	20	1	US-09-429-322-70	Sequence 70, Appl
C 738	15.6	0.2	24	1	PCT-US93-11198-187	Sequence 187, App	C 811	15.2	0.2	20	1	US-09-031-626-61	Sequence 61, Appl
C 739	15.6	0.2	30	1	US-09-725-265-5	Sequence 5, Appl	C 812	15.2	0.2	20	1	US-09-110-517-42	Sequence 42, Appl
C 740	15.6	0.2	30	1	US-09-725-265-6	Sequence 6, Appl	C 813	15.2	0.2	20	1	US-09-021-701-732	Sequence 732, App
C 741	15.6	0.2	30	1	US-09-725-265-7	Sequence 7, Appl	C 814	15.2	0.2	20	1	US-09-021-701-733	Sequence 733, App
C 742	15.6	0.2	17	1	US-08-242-664-23	Sequence 23, Appl	C 815	15.2	0.2	20	1	US-09-021-701-734	Sequence 734, App
C 743	15.4	0.2	17	1	US-08-484-138-23	Sequence 23, Appl	C 816	15.2	0.2	20	1	US-09-021-701-736	Sequence 736, App
C 744	15.4	0.2	17	1	US-08-292-620A-1931	Sequence 1931, Ap	C 817	15.2	0.2	20	1	US-09-489-765A-10	Sequence 50, App
C 745	15.4	0.2	17	1	US-09-071-845-1931	Sequence 1931, Ap	C 818	15.2	0.2	20	1	US-09-657-042A-38	Sequence 38, Appl
C 746	15.4	0.2	17	1	US-08-584-040-2884	Sequence 2884, Ap	C 819	15.2	0.2	20	1	US-09-651-011A-28	Sequence 28, Appl
C 747	15.4	0.2	17	1	US-09-371-772B-1408	Sequence 1408, Ap	C 820	15.2	0.2	20	1	US-09-536-259-9	Sequence 9, Appl
C 748	15.4	0.2	17	1	US-09-371-772B-5562	Sequence 5562, Ap	C 821	15.2	0.2	20	1	US-09-629-645A-92	Sequence 92, Appl
C 749	15.4	0.2	17	1	PCT-US95-06379-23	Sequence 23, Appl	C 822	15.2	0.2	20	1	US-09-659-791A-85	Sequence 85, Appl
C 750	15.4	0.2	18	1	US-09-140-804-18	Sequence 18, Appl	C 823	15.2	0.2	20	1	US-09-295-593-19	Sequence 19, Appl
C 751	15.4	0.2	18	1	US-09-686-838B-18	Sequence 18, Appl	C 824	15.2	0.2	20	1	US-09-676-610B-104	Sequence 104, Appl
C 752	15.4	0.2	18	1	US-09-435-019-48	Sequence 48, Appl	C 825	15.2	0.2	20	1	US-09-844-525A-45	Sequence 45, Appl
C 753	15.4	0.2	18	1	PCT-US91-03680-73	Sequence 73, Appl	C 826	15.2	0.2	20	1	US-09-725-265-40	Sequence 40, Appl
C 754	15.4	0.2	18	1	PCT-US91-03680-74	Sequence 74, Appl	C 827	15.2	0.2	20	1	US-09-725-265-41	Sequence 41, Appl
C 755	15.4	0.2	19	1	US-07-985-691-9	Sequence 9, Appl	C 828	15.2	0.2	20	1	US-09-920-759-8	Sequence 82, Appl
C 756	15.4	0.2	19	1	US-08-631-200-39	Sequence 39, Appl	C 829	15.2	0.2	20	1	US-09-920-759-889	Sequence 289, App
C 757	15.4	0.2	19	1	US-08-829-553-39	Sequence 39, Appl	C 830	15.2	0.2	20	1	US-09-402-923A-2391	Sequence 2391, App
C 758	15.4	0.2	19	1	US-08-923-257A-39	Sequence 39, Appl	C 831	15.2	0.2	20	1	US-09-198-452A-2391	Sequence 2391, App
C 759	15.4	0.2	19	1	US-08-936-707A-39	Sequence 39, Appl	C 832	15.2	0.2	20	1	US-09-198-452A-2978	Sequence 2978, Ap
C 760	15.4	0.2	19	1	US-08-936-706A-39	Sequence 39, Appl	C 833	15.2	0.2	20	1	US-09-198-452A-5002	Sequence 5002, Ap
C 761	15.4	0.2	19	1	US-09-248-203-39	Sequence 39, Appl	C 834	15.2	0.2	20	1	US-09-198-452A-5785	Sequence 5785, Ap
C 762	15.4	0.2	19	1	US-09-009-913-216	Sequence 216, App	C 835	15.2	0.2	20	1	US-09-198-452A-6476	Sequence 6476, Ap
C 763	15.4	0.2	19	1	US-09-406-071-39	Sequence 39, Appl	C 836	15.2	0.2	20	1	US-09-198-452A-6842	Sequence 6842, Ap

C 837	15.2	0.2	20	1	US-09-601-144-20	Sequence 20, Appl
C 838	15.2	0.2	20	1	US-09-823-634A-18	Sequence 18, Appl
C 839	15.2	0.2	20	1	US-09-823-647B-18	Sequence 18, Appl
C 840	15.2	0.2	20	1	US-09-780-045-104	Sequence 104, Appl
C 841	15.2	0.2	20	1	PCT-US94-02891-22	Sequence 22, Appl
C 842	15.2	0.2	21	1	US-08-145-704-11	Sequence 11, Appl
C 843	15.2	0.2	21	1	US-08-207-901-4	Sequence 4, Appl
C 844	15.2	0.2	21	1	US-08-639-501-57	Sequence 57, Appl
C 845	15.2	0.2	21	1	US-08-416-711-9	Sequence 9, Appl
C 846	15.2	0.2	21	1	US-09-044-946-57	Sequence 57, Appl
C 847	15.2	0.2	21	1	US-09-044-908-57	Sequence 57, Appl
C 848	15.2	0.2	21	1	US-08-587-574-11	Sequence 11, Appl
C 849	15.2	0.2	21	1	US-08-535-168-11	Sequence 11, Appl
C 850	15.2	0.2	21	1	US-09-017-974-11	Sequence 11, Appl
C 851	15.2	0.2	21	1	US-08-682-255A-11	Sequence 11, Appl
C 852	15.2	0.2	21	1	US-09-429-130-11	Sequence 11, Appl
C 853	15.2	0.2	21	1	US-09-227-595-14	Sequence 14, Appl
C 854	15.2	0.2	21	1	US-09-356-497-9	Sequence 9, Appl
C 855	15.2	0.2	21	1	US-09-423-978-6964	Sequence 9664, Ap
C 856	15.2	0.2	21	1	US-09-423-978-6936	Sequence 9636, Ap
C 857	15.2	0.2	21	1	US-09-422-978-11166	Sequence 11166, A
C 858	15.2	0.2	21	1	PCT-US96-11786-11	Sequence 11, Appl
C 859	15.2	0.2	22	1	US-08-457-273B-22	Sequence 22, Appl
C 860	15.2	0.2	22	1	US-08-104-165-29	Sequence 29, Appl
C 861	15.2	0.2	22	1	US-08-187-161-4	Sequence 4, Appl
C 862	15.2	0.2	22	1	US-08-464-250-29	Sequence 29, Appl
C 863	15.2	0.2	22	1	US-08-464-250-29	Sequence 29, Appl
C 864	15.2	0.2	22	1	US-09-126-980-4	Sequence 4, Appl
C 865	15.2	0.2	22	1	US-09-476-482-4	Sequence 4, Appl
C 866	15.2	0.2	22	1	US-08-897-956A-23	Sequence 23, Appl
C 867	15.2	0.2	22	1	US-09-390-134B-13	Sequence 13, Appl
C 868	15.2	0.2	22	1	US-09-780-172-11	Sequence 11, Appl
C 869	15.2	0.2	22	1	US-09-445-283C-45	Sequence 45, Appl
C 870	15.2	0.2	22	1	US-09-750-401-17	Sequence 17, Appl
C 871	15.2	0.2	22	1	US-09-750-401-19	Sequence 19, Appl
C 872	15.2	0.2	23	1	US-08-061-539-1	Sequence 1, Appl
C 873	15.2	0.2	23	1	US-08-466-647-1	Sequence 1, Appl
C 874	15.2	0.2	23	1	US-08-411-795B-1	Sequence 1, Appl
C 875	15.2	0.2	23	1	US-08-411-796-1	Sequence 1, Appl
C 876	15.2	0.2	23	1	US-08-469-319A-1	Sequence 1, Appl
C 877	15.2	0.2	23	1	US-08-378-617A-6	Sequence 6, Appl
C 878	15.2	0.2	23	1	US-08-837-302-6	Sequence 6, Appl
C 879	15.2	0.2	23	1	US-08-798-668-6	Sequence 6, Appl
C 880	15.2	0.2	23	1	US-08-471-039-1	Sequence 1, Appl
C 881	15.2	0.2	23	1	US-08-855-825-6	Sequence 6, Appl
C 882	15.2	0.2	23	1	US-09-395-345-24	Sequence 24, Appl
C 883	15.2	0.2	23	1	US-08-764-114-1	Sequence 1, Appl
C 884	15.2	0.2	23	1	US-09-091-952A-39	Sequence 39, Appl
C 885	15.2	0.2	23	1	US-08-469-419-1	Sequence 1, Appl
C 886	15.2	0.2	23	1	US-08-559-330-1	Sequence 1, Appl
C 887	15.2	0.2	23	1	US-09-419-406-6	Sequence 6, Appl
C 888	15.2	0.2	23	1	PCT-US93-11198-1	Sequence 1, Appl
C 889	15.2	0.2	29	1	US-08-666-405-15	Sequence 15, Appl
C 890	15.2	0.2	36	1	US-08-863-639A-31	Sequence 31, Appl
C 891	15	0.2	15	1	US-08-452-196A-6	Sequence 6, Appl
C 892	15	0.2	15	1	US-07-971-978-1	Sequence 1, Appl
C 893	15	0.2	15	1	US-08-756-728A-2	Sequence 2, Appl
C 894	15	0.2	15	1	US-08-663-918-3	Sequence 3, Appl
C 895	15	0.2	15	1	US-08-663-918-4	Sequence 4, Appl
C 896	15	0.2	15	1	US-08-292-620A-362	Sequence 362, App
C 897	15	0.2	15	1	US-08-771-789-3	Sequence 3, Appl
C 898	15	0.2	15	1	US-08-771-789-3	Sequence 3, Appl
C 899	15	0.2	15	1	US-08-358-556A-10	Sequence 10, Appl
C 900	15	0.2	15	1	US-08-358-556A-16	Sequence 16, Appl
C 901	15	0.2	15	1	US-08-922-170B-5	Sequence 5, Appl
C 902	15	0.2	15	1	US-08-863-639A-5	Sequence 5, Appl
C 903	15	0.2	15	1	US-08-863-639A-7	Sequence 7, Appl
C 904	15	0.2	15	1	US-08-863-639A-9	Sequence 9, Appl
C 905	15	0.2	15	1	US-08-693-831-1	Sequence 1, Appl
C 906	15	0.2	15	1	US-08-693-831-1	Sequence 1, Appl
C 907	15	0.2	15	1	US-08-832-021-62	Sequence 62, Appl
C 908	15	0.2	15	1	US-09-183-619-4	Sequence 4, Appl
C 909	15	0.2	15	1	US-09-071-645-361	Sequence 361, App
C 910	15	0.2	15	1	US-09-071-845-362	Sequence 362, App
C 911	15	0.2	15	1	US-09-142-521-3	Sequence 3, Appl
C 912	15	0.2	15	1	US-09-142-521-5	Sequence 5, Appl
C 913	15	0.2	15	1	US-09-167-975-1	Sequence 1, Appl
C 914	15	0.2	15	1	US-08-150-156A-19	Sequence 19, Appl
C 915	15	0.2	15	1	US-08-150-156A-20	Sequence 20, Appl
C 916	15	0.2	15	1	US-08-108-591B-17	Sequence 17, Appl
C 917	15	0.2	15	1	US-08-108-591B-18	Sequence 18, Appl
C 918	15	0.2	15	1	US-09-619-103-21	Sequence 21, Appl
C 919	15	0.2	15	1	US-09-300-958A-68	Sequence 68, Appl
C 920	15	0.2	15	1	US-08-988-024C-9	Sequence 9, Appl
C 921	15	0.2	15	1	US-09-435-739-5	Sequence 5, Appl
C 922	15	0.2	15	1	US-10-091-231-2	Sequence 2, Appl
C 923	15	0.2	15	1	US-09-930-218-5	Sequence 5, Appl
C 924	15	0.2	15	1	PCT-US91-03680-15	Sequence 15, Appl
C 925	15	0.2	15	1	US-09-507-345A-3	Sequence 3, Appl
C 926	15	0.2	15	1	US-09-507-345A-4	Sequence 4, Appl
C 927	15	0.2	15	1	US-09-507-345A-5	Sequence 5, Appl
C 928	15	0.2	15	1	US-09-507-345A-6	Sequence 6, Appl
C 929	15	0.2	15	1	US-09-507-345A-7	Sequence 7, Appl
C 930	15	0.2	15	1	US-09-507-345A-8	Sequence 8, Appl
C 931	15	0.2	15	1	US-09-739-928-3	Sequence 3, Appl
C 932	15	0.2	15	1	US-09-739-928-4	Sequence 4, Appl
C 933	15	0.2	15	1	US-09-739-928-5	Sequence 5, Appl
C 934	15	0.2	15	1	US-09-739-928-6	Sequence 6, Appl
C 935	15	0.2	15	1	US-09-739-928-7	Sequence 7, Appl
C 936	15	0.2	15	1	US-09-739-928-8	Sequence 8, Appl
C 937	15	0.2	15	1	US-08-584-040-2547	Sequence 2547, Ap
C 938	15	0.2	17	1	US-08-584-040-2552	Sequence 2552, Ap
C 939	15	0.2	17	1	US-09-475-447A-118	Sequence 118, Ap
C 940	15	0.2	17	1	US-09-300-958A-63	Sequence 63, Appl
C 941	15	0.2	17	1	US-09-371-772B-1071	Sequence 1071, Ap
C 942	15	0.2	17	1	US-09-371-772B-1076	Sequence 1076, Ap
C 943	15	0.2	17	1	US-09-866-108A-1537	Sequence 1537, Ap
C 944	15	0.2	17	1	US-09-866-108A-1538	Sequence 1538, Ap
C 945	15	0.2	17	1	US-09-866-108A-1539	Sequence 1539, Ap
C 946	15	0.2	18	1	US-09-487-444-11	Sequence 11, Appl
C 947	15	0.2	18	1	US-09-437-076-1	Sequence 1, Appl
C 948	15	0.2	18	1	US-09-437-076-2	Sequence 2, Appl
C 949	15	0.2	19	1	US-09-349-035-2	Sequence 2, Appl
C 950	15	0.2	20	1	US-09-593-559-9	Sequence 9, Appl
C 951	15	0.2	20	1	US-08-715-461-3	Sequence 3, Appl
C 952	15	0.2	20	1	US-08-715-461-4	Sequence 4, Appl
C 953	15	0.2	20	1	US-09-289-368-63	Sequence 63, Appl
C 954	15	0.2	20	1	US-09-844-634-57	Sequence 57, Appl
C 955	15	0.2	20	1	US-09-389-956-87	Sequence 87, Appl
C 956	15	0.2	20	1	US-09-860-473-142	Sequence 142, App
C 957	15	0.2	21	1	US-09-422-978-9155	Sequence 9155, Ap
C 958	15	0.2	23	1	US-07-918-318-19	Sequence 19, Appl
C 959	15	0.2	23	1	US-08-242-402-6	Sequence 6, Appl
C 960	15	0.2	23	1	US-08-270-180-17	Sequence 17, Appl
C 961	15	0.2	23	1	US-08-295-443-22	Sequence 22, Appl
C 962	15	0.2	23	1	US-08-682-423-17	Sequence 17, Appl
C 963	15	0.2	23	1	US-08-682-423-29	Sequence 29, Appl
C 964	15	0.2	23	1	US-09-359-756-2	Sequence 2, Appl
C 965	15	0.2	23	1	US-09-230-704-3	Sequence 3, Appl
C 966	15	0.2	23	1	US-09-609-162-3	Sequence 3, Appl
C 967	15	0.2	23	1	US-09-634-732-3	Sequence 3, Appl
C 968	15	0.2	23	1	US-09-597-771-23	Sequence 23, Appl
C 969	15	0.2	23	1	US-09-180-445-67	Sequence 67, Appl
C 970	15	0.2	23	1	US-09-364-425B-33	Sequence 33, Appl
C 971	15	0.2	23	1	US-09-860-473-13	Sequence 13, Appl
C 972	15	0.2	23	1	PCT-US95-05141-17	Sequence 17, Appl
C 973	15	0.2	23	1	PCT-US95-05141-29	Sequence 29, Appl
C 974	15	0.2	24	1	US-09-475-947B-114	Sequence 114, App
C 975	15	0.2	24	1	US-09-356-806-82	Sequence 82, Appl
C 976	15	0.2	26	1	US-08-621-914A-2	Sequence 2, Appl
C 977	15	0.2	26	1	US-08-873-437-2	Sequence 2, Appl
C 978	15	0.2	26	1	US-09-522-417-39	Sequence 39, Appl
C 979	15	0.2	26	1	US-09-593-312-3	Sequence 3, Appl
C 980	15	0.2	26	1	US-09-923-246-39	Sequence 39, Appl
C 981	15	0.2	26	1	US-09-658-077-1	Sequence 1, Appl
C 982	15	0.2	26	1	US-10-295-723-39	Sequence 39, Appl

983	15	0.2	29	1	US-10-003-998A-7	Sequence 7, Appl1	1056	14.8	0.2	20	1	US-09-485-077A-3	Sequence 3, Appl1
984	14.8	0.2	18	1	US-08-152-313-80	Sequence 80, Appl	c1057	14.8	0.2	20	1	US-09-725-265-36	Sequence 36, Appl
985	14.8	0.2	18	1	US-08-330-000-1	Sequence 80, Appl	c1058	14.8	0.2	20	1	US-09-725-265-42	Sequence 42, Appl
986	14.8	0.2	18	1	US-08-579-223-80	Sequence 80, Appl	c1059	14.8	0.2	20	1	US-09-422-978-7819	Sequence 7819, Ap
C 987	14.8	0.2	18	1	US-08-487-046-5	Sequence 5, Appl1	1060	14.8	0.2	20	1	US-09-060-299-288	Sequence 288, App
C 988	14.8	0.2	18	1	US-08-487-046-6	Sequence 6, Appl1	1061	14.8	0.2	20	1	US-09-402-923A-288	Sequence 288, App
C 989	14.8	0.2	18	1	US-08-483-522-5	Sequence 5, Appl1	1062	14.8	0.2	20	1	US-09-198-452A-4204	Sequence 4204, Ap
C 990	14.8	0.2	18	1	US-08-483-522-6	Sequence 6, Appl1	1063	14.8	0.2	20	1	US-09-254-778B-58	Sequence 28, Appl
991	14.8	0.2	18	1	US-09-213-768-17	Sequence 17, Appl1	1064	14.8	0.2	20	1	US-09-249-247-158	Sequence 158, App
992	14.8	0.2	18	1	US-09-106-038A-24	Sequence 24, Appl1	c1065	14.8	0.2	20	1	US-09-526-193A-150	Sequence 150, App
993	14.8	0.2	18	1	US-08-965-908-1	Sequence 1, Appl1	1066	14.8	0.2	20	1	US-09-980-052-146	Sequence 146, App
C 994	14.8	0.2	18	1	US-09-344-579-35	Sequence 35, Appl1	c1067	14.8	0.2	20	1	5185441-9	Sequence 146, App
C 995	14.8	0.2	18	1	US-09-199-859-49	Sequence 46, Appl1	1068	14.8	0.2	20	1	5185441-11	Sequence 46, Appl
C 996	14.8	0.2	18	1	US-08-679-645-1169	Sequence 1169, Ap	1069	14.8	0.2	21	1	US-07-977-288A-62	Sequence 62, Appl1
C 997	14.8	0.2	18	1	US-08-275-951-32	Sequence 32, Appl1	c1070	14.8	0.2	21	1	US-08-498-402-4	Sequence 4, Appl1
C 998	14.8	0.2	18	1	US-08-275-951-32	Sequence 32, Appl1	c1071	14.8	0.2	21	1	US-08-451-777A-10	Sequence 10, Appl1
C 999	14.8	0.2	18	1	US-08-275-951-32	Sequence 32, Appl1	c1072	14.8	0.2	21	1	US-08-451-778A-10	Sequence 10, Appl1
1000	14.8	0.2	18	1	US-09-475-951-33	Sequence 33, Appl1	c1073	14.8	0.2	21	1	US-08-998-208-10	Sequence 10, Appl1
c1001	14.8	0.2	18	1	US-09-475-947A-340	Sequence 340, App	1074	14.8	0.2	21	1	US-08-460-751-17	Sequence 17, Appl1
c1002	14.8	0.2	18	1	US-09-280-030-28	Sequence 28, Appl1	1075	14.8	0.2	21	1	US-08-256-426B-62	Sequence 62, Appl1
c1003	14.8	0.2	18	1	US-09-422-978-6054	Sequence 6054, Ap	1076	14.8	0.2	21	1	US-08-193-627-10	Sequence 10, Appl1
c1004	14.8	0.2	18	1	US-09-422-978-11203	Sequence 11203, A	1077	14.8	0.2	21	1	US-09-347-114A-9	Sequence 9, Appl1
c1005	14.8	0.2	18	1	US-09-856-747-46	Sequence 46, Appl1	1078	14.8	0.2	21	1	US-09-081-143-12	Sequence 12, Appl1
c1006	14.8	0.2	19	1	PCT-US94-12947A-80	Sequence 80, Appl1	c1079	14.8	0.2	21	1	US-09-598-747-21	Sequence 21, Appl1
c1007	14.8	0.2	19	1	US-08-167-113-8	Sequence 8, Appl1	1080	14.8	0.2	21	1	US-09-422-978-7056	Sequence 7056, Ap
1008	14.8	0.2	19	1	US-08-886-161-8	Sequence 8, Appl1	c1081	14.8	0.2	21	1	US-09-065-040-6	Sequence 6, Appl1
1009	14.8	0.2	19	1	US-08-899-029-1	Sequence 1, Appl1	c1082	14.8	0.2	21	1	US-09-546-986A-12	Sequence 12, Appl1
1010	14.8	0.2	19	1	US-09-422-978-5817	Sequence 5817, Ap	c1083	14.8	0.2	21	1	US-09-524-730-12	Sequence 12, Appl1
1010	14.8	0.2	20	1	US-08-502-185-27	Sequence 27, Appl1	c1084	14.8	0.2	21	1	US-09-435-733-17	Sequence 17, Appl1
1011	14.8	0.2	20	1	US-08-502-185-34	Sequence 34, Appl1	c1085	14.8	0.2	21	1	PCT-US85-06733-10	Sequence 10, Appl1
1012	14.8	0.2	20	1	US-08-502-185-37	Sequence 37, Appl1	c1086	14.8	0.2	21	1	PCT-US95-10721-4	Sequence 4, Appl1
1013	14.8	0.2	20	1	US-08-398-945-37	Sequence 37, Appl1	1087	14.8	0.2	22	1	US-08-457-272B-31	Sequence 31, Appl1
1014	14.8	0.2	20	1	US-08-398-945-34	Sequence 34, Appl1	1088	14.8	0.2	22	1	US-09-068-109-3	Sequence 3, Appl1
1015	14.8	0.2	20	1	US-08-398-945-37	Sequence 37, Appl1	c1089	14.8	0.2	22	1	US-08-538-666-14	Sequence 14, Appl1
c1016	14.8	0.2	20	1	US-08-371-121-19	Sequence 19, Appl1	c1090	14.8	0.2	22	1	US-08-538-666-20	Sequence 20, Appl1
1017	14.8	0.2	20	1	US-08-501-779-27	Sequence 27, Appl1	c1091	14.8	0.2	22	1	US-09-183-412-52	Sequence 52, Appl1
1018	14.8	0.2	20	1	US-08-501-779-34	Sequence 34, Appl1	1092	14.8	0.2	22	1	US-09-245-041-50	Sequence 50, Appl1
1019	14.8	0.2	20	1	US-08-501-779-37	Sequence 37, Appl1	c1093	14.8	0.2	22	1	US-09-769-864-52	Sequence 52, Appl1
1020	14.8	0.2	20	1	US-08-501-713-27	Sequence 27, Appl1	c1094	14.8	0.2	22	1	US-09-688-990-20	Sequence 20, Appl1
1021	14.8	0.2	20	1	US-08-501-713-34	Sequence 34, Appl1	c1095	14.8	0.2	26	1	US-08-621-914A-1	Sequence 1, Appl1
1022	14.8	0.2	20	1	US-08-501-713-37	Sequence 37, Appl1	c1096	14.8	0.2	26	1	US-09-197-951-5	Sequence 5, Appl1
1023	14.8	0.2	20	1	US-08-378-860-27	Sequence 27, Appl1	c1097	14.8	0.2	26	1	US-09-522-211-38	Sequence 38, Appl1
1024	14.8	0.2	20	1	US-08-378-860-34	Sequence 34, Appl1	c1098	14.8	0.2	26	1	US-09-527-346-7	Sequence 7, Appl1
1025	14.8	0.2	20	1	US-08-378-860-37	Sequence 37, Appl1	c1099	14.8	0.2	26	1	US-09-923-234-38	Sequence 38, Appl1
1026	14.8	0.2	20	1	US-08-501-626-27	Sequence 27, Appl1	c1100	14.8	0.2	26	1	US-10-295-723-38	Sequence 38, Appl1
1027	14.8	0.2	20	1	US-08-501-626-34	Sequence 34, Appl1	1101	14.8	0.2	28	1	US-08-762-106-11	Sequence 11, Appl1
1028	14.8	0.2	20	1	US-08-501-626-37	Sequence 37, Appl1	1102	14.8	0.2	28	1	US-09-320-774-11	Sequence 11, Appl1
1029	14.8	0.2	20	1	US-08-501-626-27	Sequence 27, Appl1	1103	14.6	0.2	21	1	US-08-146-504-2	Sequence 2, Appl1
1030	14.8	0.2	20	1	US-08-501-356-34	Sequence 34, Appl1	1104	14.6	0.2	21	1	US-08-725-976-2	Sequence 2, Appl1
1031	14.8	0.2	20	1	US-08-501-356-37	Sequence 37, Appl1	1105	14.6	0.2	21	1	US-08-271-882B-2	Sequence 2, Appl1
c1032	14.8	0.2	20	1	US-08-237-180B-46	Sequence 46, Appl1	1106	14.6	0.2	21	1	US-08-726-278-2	Sequence 2, Appl1
c1033	14.8	0.2	20	1	US-08-692-787-62	Sequence 62, Appl1	c1107	14.6	0.2	21	1	US-08-009-263C-52	Sequence 52, Appl1
c1034	14.8	0.2	20	1	US-08-837-201C-97	Sequence 97, Appl1	1108	14.6	0.2	21	1	US-08-128-011-4	Sequence 4, Appl1
c1035	14.8	0.2	20	1	US-08-904-901-158	Sequence 158, App	1109	14.6	0.2	21	1	US-07-847-055A-12	Sequence 12, Appl1
c1037	14.8	0.2	20	1	US-07-927-391-20	Sequence 20, Appl1	c1110	14.6	0.2	21	1	US-08-202-389-44	Sequence 44, Appl1
c1038	14.8	0.2	20	1	US-08-940-250-24	Sequence 24, Appl1	c1111	14.6	0.2	21	1	US-08-426-792-2	Sequence 2, Appl1
1039	14.8	0.2	20	1	US-08-858-876A-6	Sequence 6, Appl1	c1112	14.6	0.2	21	1	US-08-424-663-4	Sequence 4, Appl1
1040	14.8	0.2	20	1	US-09-357-070-24	Sequence 24, Appl1	c1113	14.6	0.2	21	1	US-08-424-663-5	Sequence 5, Appl1
1041	14.8	0.2	20	1	US-09-249-730-158	Sequence 158, App	c1114	14.6	0.2	21	1	US-08-647-351B-2	Sequence 2, Appl1
c1042	14.8	0.2	20	1	US-09-418-641-75	Sequence 75, Appl1	c1115	14.6	0.2	21	1	US-08-740-215B-1	Sequence 1, Appl1
c1043	14.8	0.2	20	1	US-09-280-799-28	Sequence 28, Appl1	1116	14.6	0.2	21	1	US-08-740-215B-4	Sequence 4, Appl1
c1044	14.8	0.2	20	1	US-09-517-584A-78	Sequence 78, Appl1	1117	14.6	0.2	21	1	US-08-403-888A-63	Sequence 63, Appl1
c1045	14.8	0.2	20	1	US-09-101-886B-77	Sequence 77, Appl1	1118	14.6	0.2	21	1	US-08-403-888A-142	Sequence 142, App
c1046	14.8	0.2	20	1	US-09-097-199-62	Sequence 62, Appl1	c1119	14.6	0.2	21	1	US-08-872-446-4	Sequence 4, Appl1
c1047	14.8	0.2	20	1	US-09-021-701-735	Sequence 735, App	c1120	14.6	0.2	21	1	US-08-872-446-5	Sequence 5, Appl1
c1048	14.8	0.2	20	1	US-09-593-711A-152	Sequence 152, App	c1121	14.6	0.2	21	1	US-08-838-718B-52	Sequence 52, Appl1
c1049	14.8	0.2	20	1	US-09-472-880-6	Sequence 6, Appl1	1122	14.6	0.2	21	1	US-08-974-549A-507	Sequence 507, App
1050	14.8	0.2	20	1	US-09-364-416-97	Sequence 97, Appl1	c1123	14.6	0.2	21	1	US-08-943-731-256	Sequence 256, App
c1051	14.8	0.2	20	1	US-09-468-872-79	Sequence 79, Appl1	1124	14.6	0.2	21	1	US-09-109-663-14	Sequence 14, Appl1
c1052	14.8	0.2	20	1	US-09-629-645A-159	Sequence 159, App	c1125	14.6	0.2	21	1	US-09-280-270A-4	Sequence 4, Appl1
c1053	14.8	0.2	20	1	US-09-561-497-87	Sequence 87, Appl1	c1126	14.6	0.2	21	1	US-09-280-270A-5	Sequence 5, Appl1
c1054	14.8	0.2	20	1	US-09-470-443-21	Sequence 21, Appl1	c1127	14.6	0.2	21	1	US-09-270-54J-96	Sequence 96, Appl1
1055	14.8	0.2	20	1	US-08-275-951-48	Sequence 48, Appl1	c1128	14.6	0.2	21	1	US-08-918-148-9	Sequence 9, Appl1

c1129	14.6	0.2	21	1	US-09-031-962D-7	Sequence 7, Appli	1202	14.4	0.2	17	1	US-08-584-040-2741	Sequence 2741, Ap
1130	14.6	0.2	21	1	US-08-912-951-274	Sequence 274, App	c1203	14.4	0.2	17	1	US-08-584-040-2885	Sequence 2885, Ap
c1131	14.6	0.2	21	1	US-09-187-288-11	Sequence 11, Appl	c1204	14.4	0.2	17	1	US-09-142-791A-7	Sequence 7, Appli
1132	14.6	0.2	21	1	US-09-187-288-12	Sequence 12, Appl	1205	14.4	0.2	17	1	US-09-371-772B-1264	Sequence 1264, Ap
c1133	14.6	0.2	21	1	US-09-255-518C-9	Sequence 9, Appli	1206	14.4	0.2	17	1	US-09-371-772B-1265	Sequence 1265, Ap
c1134	14.6	0.2	21	1	US-09-422-978-6532	Sequence 6532, Ap	c1207	14.4	0.2	17	1	US-09-371-772B-1409	Sequence 1409, Ap
c1135	14.6	0.2	21	1	US-09-422-978-8263	Sequence 8263, Ap	c1208	14.4	0.2	17	1	US-09-866-108A-2192	Sequence 2192, Ap
1136	14.6	0.2	21	1	US-09-422-978-10094	Sequence 10094, A	c1209	14.4	0.2	17	1	US-09-866-108A-2193	Sequence 2193, Ap
1137	14.6	0.2	21	1	US-09-422-978-10129	Sequence 10129, A	c1210	14.4	0.2	17	1	US-09-866-108A-2668	Sequence 2668, Ap
1138	14.6	0.2	21	1	US-09-422-978-10387	Sequence 10387, A	c1211	14.4	0.2	17	1	US-09-866-108A-2669	Sequence 2669, Ap
c1139	14.6	0.2	21	1	US-09-422-978-10387	Sequence 10387, A	c1212	14.4	0.2	17	1	US-09-866-108A-7981	Sequence 7981, Ap
1140	14.6	0.2	21	1	US-09-402-181B-507	Sequence 507, App	c1213	14.4	0.2	17	1	US-09-866-108A-7982	Sequence 7982, Ap
1141	14.6	0.2	21	1	US-09-721-456-507	Sequence 507, App	1214	14.4	0.2	18	1	US-08-488-212A-51	Sequence 51, Appl
c1142	14.6	0.2	22	1	US-08-474-140-5	Sequence 5, Appli	c1215	14.4	0.2	18	1	US-08-363-585-75	Sequence 75, Appl
c1143	14.6	0.2	22	1	US-08-477-630-5	Sequence 5, Appli	c1216	14.4	0.2	18	1	US-08-358-995-18	Sequence 18, Appl
c1144	14.6	0.2	22	1	US-08-472-293-5	Sequence 5, Appli	c1217	14.4	0.2	18	1	US-08-224-657-81	Sequence 81, Appl
c1145	14.6	0.2	22	1	US-08-474-545-5	Sequence 5, Appli	c1218	14.4	0.2	18	1	US-08-758-306-979	Sequence 979, App
c1146	14.6	0.2	22	1	US-08-358-995-22	Sequence 22, Appl	c1219	14.4	0.2	18	1	US-08-653-037A-13	Sequence 13, Appl
1147	14.6	0.2	22	1	US-08-753-147-9	Sequence 9, Appli	1220	14.4	0.2	18	1	US-08-117-952-425	Sequence 425, App
c1148	14.6	0.2	22	1	US-08-478-341-5	Sequence 5, Appli	1221	14.4	0.2	18	1	US-08-320-306-51	Sequence 51, Appl
c1149	14.6	0.2	22	1	US-08-465-590-121	Sequence 121, App	1222	14.4	0.2	18	1	US-08-488-209B-51	Sequence 51, Appl
1150	14.6	0.2	22	1	US-08-457-273B-30	Sequence 30, Appl	1223	14.4	0.2	18	1	US-08-408-011-51	Sequence 51, Appl
c1151	14.6	0.2	22	1	US-08-910-484-4	Sequence 4, Appli	1224	14.4	0.2	18	1	US-08-675-566-57	Sequence 57, Appl
c1152	14.6	0.2	22	1	US-08-766-982-8	Sequence 8, Appli	c1225	14.4	0.2	18	1	US-09-280-409-15	Sequence 35, Appl
c1153	14.6	0.2	22	1	US-08-962-790-2	Sequence 2, Appli	1226	14.4	0.2	18	1	US-09-630-706-21	Sequence 61, Appl
c1154	14.6	0.2	22	1	US-08-966-733-5	Sequence 5, Appli	c1227	14.4	0.2	18	1	US-09-354-138-81	Sequence 81, Appl
1155	14.6	0.2	22	1	US-08-781-891-81	Sequence 81, Appl	c1228	14.4	0.2	18	1	US-09-189-028-28	Sequence 28, Appl
1156	14.6	0.2	22	1	US-08-781-891-88	Sequence 88, Appl	1229	14.4	0.2	18	1	US-09-422-978-5292	Sequence 423, Ap
c1157	14.6	0.2	22	1	US-09-010-641-5	Sequence 5, Appli	c1230	14.4	0.2	18	1	US-09-920-760-43	Sequence 43, Appl
1158	14.6	0.2	22	1	US-09-147-923-7	Sequence 7, Appli	c1231	14.4	0.2	18	1	US-09-422-978-5293	Sequence 423, Ap
c1159	14.6	0.2	22	1	US-08-275-526C-19	Sequence 19, Appl	1232	14.4	0.2	18	1	US-09-422-978-5292	Sequence 5292, Ap
c1160	14.6	0.2	22	1	US-08-927-219-64	Sequence 64, Appl	1233	14.4	0.2	18	1	US-09-422-978-5292	Sequence 5292, Ap
c1161	14.6	0.2	22	1	US-09-336-281-5	Sequence 5, Appli	c1234	14.4	0.2	18	1	US-09-422-978-5292	Sequence 5292, Ap
1162	14.6	0.2	22	1	US-08-711-417C-121	Sequence 121, App	1235	14.4	0.2	19	1	US-08-967-101-171	Sequence 11, App
c1163	14.6	0.2	22	1	US-09-018-584A-95	Sequence 95, Appl	1236	14.4	0.2	19	1	US-08-592-541-171	Sequence 11, App
c1164	14.6	0.2	22	1	US-09-296-219-8	Sequence 8, Appli	1237	14.4	0.2	19	1	US-09-124-698-171	Sequence 171, App
1165	14.6	0.2	22	1	US-09-277-078-21	Sequence 21, Appl	c1238	14.4	0.2	19	1	US-09-135-621-67	Sequence 67, Appl
1166	14.6	0.2	22	1	US-08-481-659C-20	Sequence 20, Appl	1239	14.4	0.2	19	1	US-09-127-480-171	Sequence 171, App
1167	14.6	0.2	22	1	US-09-383-316-108	Sequence 108, App	1240	14.4	0.2	19	1	US-09-338-907-418	Sequence 418, App
1168	14.6	0.2	22	1	US-09-462-569B-3	Sequence 3, Appli	c1241	14.4	0.2	19	1	US-09-135-620-69	Sequence 69, Appl
c1169	14.6	0.2	22	1	US-09-076-677-19	Sequence 19, Appl	c1242	14.4	0.2	19	1	US-09-135-610A-69	Sequence 69, Appl
c1170	14.6	0.2	22	1	US-09-073-055-19	Sequence 19, Appl	c1243	14.4	0.2	19	1	US-09-444-871-69	Sequence 69, Appl
c1171	14.6	0.2	22	1	US-09-673-809-10	Sequence 10, Appl	1244	14.4	0.2	19	1	US-09-218-077-118	Sequence 418, App
c1172	14.6	0.2	22	1	US-09-589-462-7	Sequence 7, Appli	1245	14.4	0.2	19	1	US-09-124-523-171	Sequence 171, App
1173	14.6	0.2	22	1	US-09-454-495-7	Sequence 7, Appli	1246	14.4	0.2	19	1	US-09-345-882-117	Sequence 117, App
1174	14.6	0.2	22	1	US-09-618-166-81	Sequence 81, Appl	c1247	14.4	0.2	19	1	US-09-597-735-69	Sequence 69, Appl
1175	14.6	0.2	22	1	US-09-618-166-88	Sequence 88, Appl	c1248	14.4	0.2	19	1	US-09-444-895-69	Sequence 69, Appl
1176	14.6	0.2	22	1	US-09-168-947-46	Sequence 46, Appl	c1249	14.4	0.2	19	1	US-09-597-732-69	Sequence 69, Appl
1177	14.6	0.2	22	1	US-09-180-245-35	Sequence 25, Appl	1250	14.4	0.2	19	1	US-09-636-796A-171	Sequence 171, App
1178	14.6	0.2	22	1	US-09-180-245-27	Sequence 27, Appl	1251	14.4	0.2	19	1	US-09-422-978-5006	Sequence 5006, App
1179	14.6	0.2	22	1	US-09-180-245-29	Sequence 29, Appl	c1252	14.4	0.2	19	1	US-09-422-978-6457	Sequence 6457, Ap
1180	14.6	0.2	22	1	US-09-180-245-31	Sequence 31, Appl	1253	14.4	0.2	19	1	US-09-422-978-8352	Sequence 8352, Ap
1181	14.6	0.2	22	1	US-09-180-245-33	Sequence 33, Appl	1254	14.4	0.2	19	1	US-09-060-399-54	Sequence 54, Appl
1182	14.6	0.2	22	1	US-09-180-245-35	Sequence 35, Appl	1255	14.4	0.2	19	1	US-09-422-978-8352	Sequence 8352, Ap
1183	14.6	0.2	22	1	US-09-180-245-37	Sequence 37, Appl	c1256	14.4	0.2	19	1	US-09-597-731-69	Sequence 69, Appl
c1184	14.6	0.2	22	1	US-09-723-909-121	Sequence 121, App	c1257	14.4	0.2	20	1	US-08-317-648-3	Sequence 3, Appli
c1185	14.6	0.2	22	1	PCT-US93-08743-121	Sequence 121, App	1258	14.4	0.2	20	1	US-08-502-185-12	Sequence 12, Appl
1186	14.6	0.2	25	1	US-09-866-108A-13467	Sequence 2, Appli	1259	14.4	0.2	20	1	US-08-398-945-12	Sequence 12, Appl
c1187	14.6	0.2	30	1	US-08-771-781-2	Sequence 70, Appl	c1261	14.4	0.2	20	1	US-08-501-779-12	Sequence 12, Appl
c1188	14.4	0.2	16	1	US-09-479-005A-70	Sequence 76, App	1262	14.4	0.2	20	1	US-08-376-162A-8	Sequence 8, Appli
c1189	14.4	0.2	17	1	US-08-373-124A-736	Sequence 972, App	c1263	14.4	0.2	20	1	US-08-588-821-71	Sequence 71, Appl
c1190	14.4	0.2	17	1	US-08-373-124A-1965	Sequence 1965, Ap	1264	14.4	0.2	20	1	US-08-860-13	Sequence 12, Appl
c1191	14.4	0.2	17	1	US-08-373-124A-2053	Sequence 2053, Ap	c1265	14.4	0.2	20	1	US-08-217-082A-3	Sequence 3, Appli
c1192	14.4	0.2	17	1	US-08-373-124A-2143	Sequence 2143, Ap	1266	14.4	0.2	20	1	US-08-501-126-12	Sequence 12, Appl
1193	14.4	0.2	17	1	US-08-373-124A-2145	Sequence 2145, Ap	c1267	14.4	0.2	20	1	US-08-915-214-71	Sequence 71, Appl
c1195	14.4	0.2	17	1	US-08-435-628-736	Sequence 736, App	1268	14.4	0.2	20	1	US-08-501-356-12	Sequence 12, Appl
c1196	14.4	0.2	17	1	US-08-435-628-972	Sequence 972, App	c1269	14.4	0.2	20	1	US-08-465-885A-3	Sequence 32, Appli
1197	14.4	0.2	17	1	US-08-435-628-1965	Sequence 1965, Ap	c1270	14.4	0.2	20	1	US-08-229-528-32	Sequence 32, Appli
c1198	14.4	0.2	17	1	US-08-435-628-2053	Sequence 2053, Ap	c1271	14.4	0.2	20	1	US-09-005-532-71	Sequence 71, Appl
1199	14.4	0.2	17	1	US-08-435-628-2143	Sequence 2143, Ap	c1272	14.4	0.2	20	1	US-09-080-285-3	Sequence 12, Appl
1200	14.4	0.2	17	1	US-08-435-628-2145	Sequence 2145, Ap	1273	14.4	0.2	20	1	US-08-987-326-121	Sequence 12, Appl
1201	14.4	0.2	17	1	US-08-584-040-2740	Sequence 2740, Ap	c1274	14.4	0.2	20	1	US-09-166-186-221	Sequence 221, App

c1275	14.4	0.2	20	1	US-08-882-046-74	Sequence 74, Appl	1348	14.2	0.2	16	1	US-08-882-649A-8	Sequence 8, Appl1
1276	14.4	0.2	20	1	US-09-286-904-76	Sequence 76, Appl	c1349	14.2	0.2	19	1	US-08-701-380-5	Sequence 5, Appl1
c1277	14.4	0.2	20	1	US-09-429-323-78	Sequence 78, Appl	1350	14.2	0.2	19	1	US-08-851-135-1	Sequence 1, Appl1
1278	14.4	0.2	20	1	US-08-765-340-26	Sequence 26, Appl	1351	14.2	0.2	19	1	US-08-996-306-46	Sequence 46, Appl
c1279	14.4	0.2	20	1	US-09-359-756-31	Sequence 31, Appl	1352	14.2	0.2	19	1	US-08-832-078-3	Sequence 3, Appl1
c1280	14.4	0.2	20	1	US-09-435-296-26	Sequence 26, Appl	c1353	14.2	0.2	19	1	US-09-032-365A-39	Sequence 39, Appl1
c1281	14.4	0.2	20	1	US-09-358-683-26	Sequence 26, Appl	1354	14.2	0.2	19	1	US-09-338-907-46	Sequence 46, Appl
c1282	14.4	0.2	20	1	US-09-313-932-221	Sequence 221, App	1355	14.2	0.2	19	1	US-09-338-907-380	Sequence 380, App
c1283	14.4	0.2	20	1	US-09-313-932-366	Sequence 366, App	1356	14.2	0.2	19	1	US-09-218-207-46	Sequence 46, App
1284	14.4	0.2	20	1	US-09-021-701-727	Sequence 727, App	1357	14.2	0.2	19	1	US-09-218-207-360	Sequence 380, App
1285	14.4	0.2	20	1	US-08-906-156A-87	Sequence 87, Appl	c1358	14.2	0.2	19	1	US-09-531-000-21	Sequence 21, Appl
c1286	14.4	0.2	20	1	US-09-489-765A-25	Sequence 25, Appl	c1359	14.2	0.2	19	1	US-09-422-978-4116	Sequence 4116, Ap
c1287	14.4	0.2	20	1	US-09-489-765A-25	Sequence 25, Appl	c1360	14.2	0.2	19	1	US-09-422-978-6486	Sequence 6486, Ap
c1288	14.4	0.2	20	1	US-09-798-096-67	Sequence 67, Appl	1361	14.2	0.2	19	1	US-09-422-978-7856	Sequence 7856, Ap
1289	14.4	0.2	20	1	US-09-724-426-3	Sequence 3, Appl1	1362	14.2	0.2	19	1	US-09-422-978-11738	Sequence 11738, A
1290	14.4	0.2	20	1	US-09-658-679A-50	Sequence 50, Appl	c1363	14.2	0.2	20	1	US-08-108-591B-4	Sequence 4, Appl1
1291	14.4	0.2	20	1	US-09-658-679A-51	Sequence 51, Appl	1363	14.2	0.2	20	1	US-07-952-44-21	Sequence 21, Appl
c1292	14.4	0.2	20	1	US-09-640-101-76	Sequence 76, Appl	c1364	14.2	0.2	20	1	US-08-138-608-53	Sequence 53, Appl
c1293	14.4	0.2	20	1	US-08-626-285-48	Sequence 48, Appl	1365	14.2	0.2	20	1	US-07-984-044A-8	Sequence 8, Appl1
c1294	14.4	0.2	20	1	US-09-668-113A-118	Sequence 118, App	1366	14.2	0.2	20	1	US-08-142-845-12	Sequence 12, Appl
1295	14.4	0.2	20	1	US-09-422-978-5670	Sequence 5670, Ap	c1367	14.2	0.2	20	1	US-08-142-845-16	Sequence 16, Appl
1296	14.4	0.2	20	1	US-09-422-978-9656	Sequence 9656, Ap	1368	14.2	0.2	20	1	US-08-117-328-4	Sequence 4, Appl1
c1297	14.4	0.2	20	1	US-09-973-959-2	Sequence 2, Appl1	1369	14.2	0.2	20	1	US-08-117-328-4	Sequence 4, Appl1
c1298	14.4	0.2	20	1	US-09-705-267A-152	Sequence 152, App	c1370	14.2	0.2	20	1	US-08-250-856A-28	Sequence 28, Appl
c1299	14.4	0.2	20	1	US-09-198-452A-1513	Sequence 1513, Ap	c1371	14.2	0.2	20	1	US-08-179-738-22	Sequence 22, Appl
c1300	14.4	0.2	20	1	US-09-198-452A-1915	Sequence 1915, Ap	1372	14.2	0.2	20	1	US-08-222-177A-240	Sequence 240, App
c1301	14.4	0.2	20	1	US-09-198-452A-3250	Sequence 3250, Ap	c1373	14.2	0.2	20	1	US-08-269-766-21	Sequence 21, Appl
c1302	14.4	0.2	20	1	US-09-198-452A-3452	Sequence 3452, Ap	1374	14.2	0.2	20	1	US-08-479-487-76	Sequence 76, Appl
c1303	14.4	0.2	20	1	US-09-198-452A-3870	Sequence 3870, Ap	c1375	14.2	0.2	20	1	US-07-951-715A-57	Sequence 57, Appl
c1304	14.4	0.2	20	1	US-09-808-358-18	Sequence 18, Appl	1376	14.2	0.2	20	1	US-08-412-431-4	Sequence 4, Appl1
c1305	14.4	0.2	20	1	US-09-808-358-44	Sequence 44, Appl	c1377	14.2	0.2	20	1	US-08-429-181-61	Sequence 61, Appl
1306	14.4	0.2	20	1	US-09-679-299A-52	Sequence 52, Appl	1378	14.2	0.2	20	1	US-08-088-658-31	Sequence 31, Appl
1307	14.4	0.2	20	1	US-08-988-024C-16	Sequence 16, Appl	c1379	14.2	0.2	20	1	US-08-088-658-31	Sequence 31, Appl
1308	14.4	0.2	20	1	US-08-988-024C-26	Sequence 26, Appl	1380	14.2	0.2	20	1	US-08-458-339-8	Sequence 8, Appl1
1309	14.4	0.2	20	1	US-08-988-024C-27	Sequence 27, Appl	1381	14.2	0.2	20	1	US-08-623-677-4	Sequence 4, Appl1
1310	14.4	0.2	21	1	US-08-457-176-11	Sequence 11, Appl	c1382	14.2	0.2	20	1	US-08-164-388-61	Sequence 61, Appl
c1311	14.4	0.2	21	1	US-08-457-175-11	Sequence 11, Appl	1383	14.2	0.2	20	1	US-08-487-141B-18	Sequence 18, Appl
c1312	14.4	0.2	21	1	US-08-753-147-86	Sequence 86, Appl	1384	14.2	0.2	20	1	US-08-487-141B-18	Sequence 18, Appl
1313	14.4	0.2	21	1	US-07-662-764D-12	Sequence 12, Appl	c1385	14.2	0.2	20	1	US-08-507-431-35	Sequence 35, Appl
c1314	14.4	0.2	21	1	US-09-121-887-6	Sequence 6, Appl1	1386	14.2	0.2	20	1	US-08-417-476-39	Sequence 39, Appl
c1315	14.4	0.2	21	1	US-09-241-953-6	Sequence 6, Appl1	1387	14.2	0.2	20	1	US-08-751-282-1	Sequence 1, Appl1
c1316	14.4	0.2	21	1	US-09-245-984-6	Sequence 6, Appl1	c1388	14.2	0.2	20	1	US-08-751-282-1	Sequence 1, Appl1
1317	14.4	0.2	21	1	US-08-989-251-21	Sequence 21, Appl	1389	14.2	0.2	20	1	US-08-186-223-55	Sequence 55, Appl
c1318	14.4	0.2	21	1	US-09-241-979-6	Sequence 6, Appl1	c1390	14.2	0.2	20	1	US-08-319-545A-21	Sequence 21, Appl
1319	14.4	0.2	21	1	US-09-340-250-21	Sequence 21, Appl	1391	14.2	0.2	20	1	US-08-531-556-35	Sequence 35, Appl
c1320	14.4	0.2	21	1	US-08-974-549A-470	Sequence 470, App	1392	14.2	0.2	20	1	US-08-472-418-35	Sequence 35, Appl
1321	14.4	0.2	21	1	US-09-045-054-13	Sequence 13, Appl	1393	14.2	0.2	20	1	US-08-512-681-22	Sequence 22, Appl
1322	14.4	0.2	21	1	US-09-528-108-21	Sequence 21, Appl	c1394	14.2	0.2	20	1	US-08-227-108-21	Sequence 21, Appl
1323	14.4	0.2	21	1	US-08-649-950-77	Sequence 77, Appl	1395	14.2	0.2	20	1	US-08-465-485A-28	Sequence 28, Appl
c1324	14.4	0.2	21	1	US-08-912-951-237	Sequence 237, App	1397	14.2	0.2	20	1	US-08-628-4-13	Sequence 13, Appl
c1325	14.4	0.2	21	1	US-09-659-845A-12	Sequence 12, Appl	c1398	14.2	0.2	20	1	US-08-470-124-55	Sequence 55, Appl
1326	14.4	0.2	21	1	US-09-193-390A-12	Sequence 12, Appl	c1399	14.2	0.2	20	1	US-08-459-448A-57	Sequence 57, Appl
c1327	14.4	0.2	21	1	US-09-402-181B-470	Sequence 470, App	c1400	14.2	0.2	20	1	US-08-808-550-16	Sequence 16, Appl
c1328	14.4	0.2	21	1	US-09-721-456-470	Sequence 470, App	c1401	14.2	0.2	20	1	US-08-628-14-22	Sequence 22, Appl
1329	14.4	0.2	22	1	US-09-526-193A-188	Sequence 188, App	1402	14.2	0.2	20	1	US-08-927-561-18	Sequence 18, Appl
c1330	14.4	0.2	22	1	US-08-611-155B-1	Sequence 1, Appl1	c1403	14.2	0.2	20	1	US-08-927-561-19	Sequence 19, Appl
c1331	14.4	0.2	22	1	US-08-611-155B-2	Sequence 2, Appl1	c1404	14.2	0.2	20	1	US-07-923-871C-5	Sequence 5, Appl1
c1332	14.4	0.2	22	1	US-08-611-155B-6	Sequence 6, Appl1	1405	14.2	0.2	20	1	US-08-954-391-1	Sequence 1, Appl1
c1333	14.4	0.2	22	1	US-08-231-894A-3	Sequence 3, Appl1	c1406	14.2	0.2	20	1	US-08-954-391-1	Sequence 1, Appl1
c1334	14.4	0.2	22	1	US-08-916-120A-1	Sequence 1, Appl1	1407	14.2	0.2	20	1	US-09-116-780-8	Sequence 8, Appl1
c1335	14.4	0.2	22	1	US-08-916-120A-2	Sequence 2, Appl1	c1408	14.2	0.2	20	1	US-08-756-806A-28	Sequence 28, Appl
c1336	14.4	0.2	22	1	US-08-916-120A-6	Sequence 6, Appl1	1409	14.2	0.2	20	1	US-08-476-712-2	Sequence 2, Appl1
1337	14.4	0.2	22	1	US-08-545-196B-36	Sequence 36, Appl	c1410	14.2	0.2	20	1	US-09-048-804-2	Sequence 2, Appl1
c1338	14.4	0.2	22	1	US-08-943-731-557	Sequence 557, App	c1411	14.2	0.2	20	1	US-08-665-202-127	Sequence 127, App
c1339	14.4	0.2	22	1	US-09-564-805-198	Sequence 198, App	c1412	14.2	0.2	20	1	US-08-968-54C-8	Sequence 8, Appl1
c1340	14.4	0.2	22	1	US-09-862-660-14	Sequence 14, Appl	1413	14.2	0.2	20	1	US-08-471-907A-31	Sequence 31, Appl
c1341	14.4	0.2	22	1	US-09-862-660-14	Sequence 14, Appl	c1414	14.2	0.2	20	1	US-08-471-907A-31	Sequence 31, Appl
c1342	14.4	0.2	24	1	US-09-721-154-4	Sequence 4, Appl1	c1415	14.2	0.2	20	1	US-09-092-988-21	Sequence 21, Appl
c1343	14.4	0.2	24	1	US-09-721-154-1	Sequence 1, Appl1	c1416	14.2	0.2	20	1	US-09-073-674-21	Sequence 21, Appl
c1344	14.4	0.2	24	1	US-08-487-799-17	Sequence 17, Appl	c1417	14.2	0.2	20	1	US-08-904-901-132	Sequence 132, App
c1345	14.4	0.2	26	1	US-08-747-536-17	Sequence 17, Appl	c1418	14.2	0.2	20	1	US-08-914-961-6	Sequence 6, Appl1
c1346	14.4	0.2	29	1	US-09-304-232-152	Sequence 152, App	c1419	14.2	0.2	20	1	US-08-459-592A-57	Sequence 57, Appl
c1347	14.2	0.2	15	1	US-08-882-649A-7	Sequence 7, Appl1	c1420	14.2	0.2	20	1	US-08-483-746A-13	Sequence 13, Appl

1421	14.2	0.2	20	1	US-08-483-746A-17	Sequence 17, Appl	c1494	14.2	0.2	20	1	US-09-702-246-39	Sequence 39, Appl
1422	14.2	0.2	20	1	US-08-933-774-4	Sequence 4, Appl	c1495	14.2	0.2	20	1	US-09-044-781B-14	Sequence 14, Appl
1423	14.2	0.2	20	1	US-09-080-285-28	Sequence 28, Appl	c1496	14.2	0.2	20	1	US-09-387-341-223	Sequence 223, Appl
1424	14.2	0.2	20	1	US-09-289-267-96	Sequence 96, Appl	1497	14.2	0.2	20	1	US-09-851-896-84	Sequence 84, Appl
c1425	14.2	0.2	20	1	US-08-417-089-10	Sequence 10, Appl	c1498	14.2	0.2	20	1	US-09-506-073-30	Sequence 30, Appl
1426	14.2	0.2	20	1	US-08-441-971-147	Sequence 147, Appl	1499	14.2	0.2	20	1	US-09-724-426-28	Sequence 28, Appl
c1427	14.2	0.2	20	1	US-08-459-504B-57	Sequence 57, Appl	c1500	14.2	0.2	20	1	US-08-697-826A-7	Sequence 7, Appl
c1428	14.2	0.2	20	1	US-09-116-622-35	Sequence 35, Appl	c1501	14.2	0.2	20	1	US-09-597-735-29	Sequence 29, Appl
1429	14.2	0.2	20	1	US-09-166-186-68	Sequence 68, Appl	1502	14.2	0.2	20	1	US-09-657-452A-72	Sequence 72, Appl
1430	14.2	0.2	20	1	US-09-166-186-130	Sequence 130, Appl	c1503	14.2	0.2	20	1	US-09-702-327-65	Sequence 65, Appl
c1331	14.2	0.2	20	1	US-09-143-214-28	Sequence 28, Appl	c1504	14.2	0.2	20	1	US-09-444-295-29	Sequence 29, Appl
c1332	14.2	0.2	20	1	US-09-000-136-14	Sequence 14, Appl	c1505	14.2	0.2	20	1	US-09-780-175-132	Sequence 132, Appl
c1333	14.2	0.2	20	1	US-08-545-809A-72	Sequence 72, Appl	1506	14.2	0.2	20	1	US-09-907-443-39	Sequence 29, Appl
c1334	14.2	0.2	20	1	US-09-344-914-72	Sequence 72, Appl	c1507	14.2	0.2	20	1	US-09-907-843-87	Sequence 87, Appl
c1335	14.2	0.2	20	1	US-09-344-914-73	Sequence 73, Appl	1508	14.2	0.2	20	1	US-09-470-443-113	Sequence 113, Appl
c1336	14.2	0.2	20	1	US-09-249-730-132	Sequence 132, Appl	c1509	14.2	0.2	20	1	US-09-658-679A-66	Sequence 66, Appl
c1437	14.2	0.2	20	1	US-08-459-444-57	Sequence 57, Appl	1510	14.2	0.2	20	1	US-09-676-610B-60	Sequence 60, Appl
1438	14.2	0.2	20	1	US-09-418-641-12	Sequence 12, Appl	c1511	14.2	0.2	20	1	US-09-676-610B-118	Sequence 118, Appl
1439	14.2	0.2	20	1	US-09-091-899-8	Sequence 8, Appl	c1512	14.2	0.2	20	1	US-09-853-768-44	Sequence 44, Appl
c1440	14.2	0.2	20	1	US-08-695-651-10	Sequence 10, Appl	1513	14.2	0.2	20	1	US-09-328-174A-83	Sequence 83, Appl
c1441	14.2	0.2	20	1	US-08-765-340-35	Sequence 35, Appl	1514	14.2	0.2	20	1	US-09-328-174A-84	Sequence 84, Appl
1442	14.2	0.2	20	1	US-08-765-340-90	Sequence 90, Appl	1515	14.2	0.2	20	1	US-09-791-211-66	Sequence 66, Appl
c1443	14.2	0.2	20	1	US-09-135-021-27	Sequence 27, Appl	c1516	14.2	0.2	20	1	US-09-441-340-22	Sequence 22, Appl
c1444	14.2	0.2	20	1	US-09-106-216-21	Sequence 21, Appl	c1517	14.2	0.2	20	1	US-09-597-732-29	Sequence 29, Appl
c1445	14.2	0.2	20	1	US-09-429-034-21	Sequence 21, Appl	c1518	14.2	0.2	20	1	US-09-746-694-42	Sequence 42, Appl
c1446	14.2	0.2	20	1	US-09-433-699-64	Sequence 64, Appl	c1519	14.2	0.2	20	1	US-09-517-467B-58	Sequence 58, Appl
1447	14.2	0.2	20	1	US-09-428-219-15	Sequence 15, Appl	c1520	14.2	0.2	20	1	US-09-091-952A-58	Sequence 58, Appl
c1448	14.2	0.2	20	1	US-09-490-692-167	Sequence 167, Appl	1521	14.2	0.2	20	1	US-09-360-416-43	Sequence 43, Appl
1449	14.2	0.2	20	1	US-09-488-671-98	Sequence 98, Appl	c1522	14.2	0.2	20	1	US-09-780-049-25	Sequence 25, Appl
c1450	14.2	0.2	20	1	US-09-517-584A-63	Sequence 63, Appl	1523	14.2	0.2	20	1	US-09-305-856B-71	Sequence 71, Appl
c1451	14.2	0.2	20	1	US-08-766-528-68	Sequence 68, Appl	1524	14.2	0.2	20	1	US-09-305-856B-73	Sequence 73, Appl
1452	14.2	0.2	20	1	US-08-221-653-147	Sequence 147, Appl	c1525	14.2	0.2	20	1	US-09-725-265-34	Sequence 34, Appl
c1453	14.2	0.2	20	1	US-09-219-277-35	Sequence 35, Appl	c1526	14.2	0.2	20	1	US-09-658-688A-21	Sequence 21, Appl
1454	14.2	0.2	20	1	US-09-253-025-6	Sequence 6, Appl	c1527	14.2	0.2	20	1	US-09-657-346A-151	Sequence 151, Appl
c1455	14.2	0.2	20	1	US-08-442-144A-147	Sequence 147, Appl	c1528	14.2	0.2	20	1	US-09-668-113A-44	Sequence 44, Appl
c1456	14.2	0.2	20	1	US-09-446-504-31	Sequence 31, Appl	c1529	14.2	0.2	20	1	US-09-315-574-127	Sequence 127, Appl
c1457	14.2	0.2	20	1	US-08-930-285-10	Sequence 10, Appl	c1530	14.2	0.2	20	1	US-08-754-477A-92	Sequence 92, Appl
c1458	14.2	0.2	20	1	US-08-930-285-24	Sequence 24, Appl	1531	14.2	0.2	20	1	US-09-422-978-4737	Sequence 4737, Appl
c1459	14.2	0.2	20	1	US-09-476-256-12	Sequence 12, Appl	1532	14.2	0.2	20	1	US-09-422-978-8838	Sequence 8838, Appl
c1460	14.2	0.2	20	1	US-09-476-256-7	Sequence 7, Appl	1533	14.2	0.2	20	1	US-09-422-978-10868	Sequence 10868, A
c1461	14.2	0.2	20	1	US-09-599-661-35	Sequence 35, Appl	c1534	14.2	0.2	20	1	US-08-687-636-11	Sequence 11, Appl
1462	14.2	0.2	20	1	US-09-313-932-68	Sequence 68, Appl	1535	14.2	0.2	20	1	US-09-198-452A-1307	Sequence 1307, Appl
c1463	14.2	0.2	20	1	US-09-313-932-130	Sequence 130, Appl	1536	14.2	0.2	20	1	US-09-198-452A-1575	Sequence 1575, Appl
c1464	14.2	0.2	20	1	US-09-313-932-297	Sequence 297, Appl	1537	14.2	0.2	20	1	US-09-198-452A-1859	Sequence 1859, Appl
1465	14.2	0.2	20	1	US-08-427-569-55	Sequence 55, Appl	c1538	14.2	0.2	20	1	US-09-198-452A-1958	Sequence 1958, Appl
c1466	14.2	0.2	20	1	US-09-560-594-59	Sequence 59, Appl	c1539	14.2	0.2	20	1	US-09-198-452A-2176	Sequence 2176, Appl
c1467	14.2	0.2	20	1	US-09-021-701-669	Sequence 669, Appl	c1540	14.2	0.2	20	1	US-09-198-452A-2534	Sequence 2534, Appl
c1468	14.2	0.2	20	1	US-09-021-701-670	Sequence 670, Appl	1541	14.2	0.2	20	1	US-09-198-452A-2989	Sequence 2989, Appl
1469	14.2	0.2	20	1	US-09-021-701-737	Sequence 737, Appl	1542	14.2	0.2	20	1	US-09-198-452A-3434	Sequence 3434, Appl
1470	14.2	0.2	20	1	US-09-021-701-773	Sequence 773, Appl	1543	14.2	0.2	20	1	US-09-198-452A-4619	Sequence 4619, Appl
1471	14.2	0.2	20	1	US-09-021-701-774	Sequence 774, Appl	1544	14.2	0.2	20	1	US-09-198-452A-4967	Sequence 4967, Appl
c1472	14.2	0.2	20	1	US-09-181-030-4	Sequence 4, Appl	1545	14.2	0.2	20	1	US-09-198-452A-5175	Sequence 5175, Appl
c1473	14.2	0.2	20	1	US-09-489-869-15	Sequence 15, Appl	1546	14.2	0.2	20	1	US-09-198-452A-6067	Sequence 6067, Appl
c1474	14.2	0.2	20	1	US-08-695-421-10	Sequence 10, Appl	c1547	14.2	0.2	20	1	US-09-198-452A-6287	Sequence 6287, Appl
1475	14.2	0.2	20	1	US-09-593-711A-54	Sequence 54, Appl	c1548	14.2	0.2	20	1	US-09-198-452A-6290	Sequence 6290, Appl
c1476	14.2	0.2	20	1	US-09-593-711A-228	Sequence 228, Appl	c1549	14.2	0.2	20	1	US-09-198-452A-6683	Sequence 6683, Appl
c1477	14.2	0.2	20	1	US-09-135-020-29	Sequence 29, Appl	c1550	14.2	0.2	20	1	US-09-597-731-29	Sequence 29, Appl
1478	14.2	0.2	20	1	US-09-230-804-6	Sequence 6, Appl	1551	14.2	0.2	20	1	US-09-909-595-83	Sequence 83, Appl
c1479	14.2	0.2	20	1	US-09-135-010A-29	Sequence 29, Appl	c1552	14.2	0.2	20	1	US-09-249-247-132	Sequence 132, Appl
1480	14.2	0.2	20	1	US-08-441-970-147	Sequence 147, Appl	1553	14.2	0.2	20	1	US-10-072-094-105	Sequence 105, Appl
1481	14.2	0.2	20	1	US-08-169-715-56	Sequence 56, Appl	c1554	14.2	0.2	20	1	US-09-780-045-37	Sequence 37, Appl
1482	14.2	0.2	20	1	US-09-411-291-2	Sequence 2, Appl	1555	14.2	0.2	20	1	US-09-780-045-93	Sequence 93, Appl
c1483	14.2	0.2	20	1	US-09-721-822A-90	Sequence 90, Appl	c1556	14.2	0.2	20	1	US-09-112-580-41	Sequence 41, Appl
1484	14.2	0.2	20	1	US-09-534-242-4	Sequence 4, Appl	c1557	14.2	0.2	20	1	US-09-554-467A-8	Sequence 8, Appl
1485	14.2	0.2	20	1	US-09-454-854-4	Sequence 4, Appl	1558	14.2	0.2	20	1	US-09-554-726A-29	Sequence 29, Appl
c1486	14.2	0.2	20	1	US-09-547-422-57	Sequence 57, Appl	1559	14.2	0.2	20	1	US-09-734-188-6	Sequence 6, Appl
c1487	14.2	0.2	20	1	US-09-444-871-29	Sequence 29, Appl	c1560	14.2	0.2	20	1	PCT-US91-0157A-5	Sequence 77, Appl
c1488	14.2	0.2	20	1	US-09-712-266-31	Sequence 31, Appl	c1561	14.2	0.2	20	1	PCT-US93-0774A-14	Sequence 14, Appl
c1489	14.2	0.2	20	1	US-09-651-011A-14	Sequence 14, Appl	c1562	14.2	0.2	20	1	PCT-US95-07111A-18	Sequence 18, Appl
1490	14.2	0.2	20	1	US-09-388-349-10	Sequence 10, Appl	c1563	14.2	0.2	20	1	PCT-US96-09388-18	Sequence 18, Appl
1491	14.2	0.2	20	1	US-09-662-250A-68	Sequence 68, Appl	1564	14.2	0.2	20	1	PCT-US96-09388-19	Sequence 19, Appl
1492	14.2	0.2	20	1	US-09-164-671-4	Sequence 4, Appl	1565	14.2	0.2	20	1	US-08-424-663-5	Sequence 5, Appl
1493	14.2	0.2	20	1	US-09-177-437-8	Sequence 8, Appl	1566	14.2	0.2	21	1		

1567	14.2	0.2	21	1	US-08-872-446-5	Sequence 5, Appl1	1640	14.2	0.2	21	1	US-09-422-978-10757	Sequence 10757, A
1568	14.2	0.2	21	1	US-09-280-270A-5	Sequence 5, Appl1	1641	14.2	0.2	21	1	US-09-422-978-11155	Sequence 11155, A
1569	14.2	0.2	21	1	US-07-873-915A-1	Sequence 1, Appl1	1642	14.2	0.2	21	1	US-09-422-978-11515	Sequence 11515, A
1570	14.2	0.2	21	1	US-07-932-379A-19	Sequence 19, Appl1	1643	14.2	0.2	21	1	US-09-422-978-11524	Sequence 11524, A
1571	14.2	0.2	21	1	US-08-042-747A-2	Sequence 2, Appl1	1644	14.2	0.2	21	1	US-09-404-641-29	Sequence 29, Appl1
1572	14.2	0.2	21	1	US-08-063-167A-36	Sequence 36, Appl1	1645	14.2	0.2	21	1	US-09-175-684A-16	Sequence 16, Appl1
1573	14.2	0.2	21	1	US-08-379-295-19	Sequence 19, Appl1	1646	14.2	0.2	21	1	US-09-923-246-11	Sequence 11, Appl1
1574	14.2	0.2	21	1	US-08-257-964-1	Sequence 1, Appl1	1647	14.2	0.2	21	1	US-09-923-246-51	Sequence 51, Appl1
1575	14.2	0.2	21	1	US-08-379-296-19	Sequence 19, Appl1	1648	14.2	0.2	21	1	US-09-402-181B-514	Sequence 514, App
1576	14.2	0.2	21	1	US-08-136-118-3	Sequence 3, Appl1	1649	14.2	0.2	21	1	US-09-721-456-514	Sequence 514, App
1577	14.2	0.2	21	1	US-08-007-997A-36	Sequence 36, Appl1	1650	14.2	0.2	21	1	US-09-486-147-19	Sequence 19, Appl1
1578	14.2	0.2	21	1	US-08-076-090-3	Sequence 3, Appl1	1651	14.2	0.2	21	1	US-09-723-909-34	Sequence 34, Appl1
1579	14.2	0.2	21	1	US-08-076-090-4	Sequence 4, Appl1	1652	14.2	0.2	21	1	US-09-908-410-9	Sequence 9, Appl1
1580	14.2	0.2	21	1	US-08-445-746-6	Sequence 6, Appl1	1653	14.2	0.2	21	1	US-09-726-774-54	Sequence 54, Appl1
1581	14.2	0.2	21	1	US-08-438-639-1	Sequence 1, Appl1	1654	14.2	0.2	21	1	US-09-726-774-73	Sequence 73, Appl1
1582	14.2	0.2	21	1	US-08-446-600A-6	Sequence 6, Appl1	1655	14.2	0.2	21	1	US-09-077-773-19	Sequence 19, Appl1
1583	14.2	0.2	21	1	US-07-813-338A-1	Sequence 1, Appl1	1656	14.2	0.2	21	1	US-09-870-958-27	Sequence 27, Appl1
1584	14.2	0.2	21	1	US-08-211-430-8	Sequence 8, Appl1	1657	14.2	0.2	21	1	US-10-065-135A-60	Sequence 60, Appl1
1585	14.2	0.2	21	1	US-08-753-147-24	Sequence 24, Appl1	1658	14.2	0.2	21	1	US-10-295-723-51	Sequence 11, Appl1
1586	14.2	0.2	21	1	US-08-592-936B-19	Sequence 19, Appl1	1659	14.2	0.2	21	1	PCT-US93-08101-36	Sequence 36, Appl1
1587	14.2	0.2	21	1	US-08-110-691A-30	Sequence 30, Appl1	1660	14.2	0.2	21	1	PCT-US94-06661-3	Sequence 3, Appl1
1588	14.2	0.2	21	1	US-08-465-590-34	Sequence 34, Appl1	1661	14.2	0.2	21	1	PCT-US94-06661-4	Sequence 4, Appl1
1589	14.2	0.2	21	1	US-08-472-659-27	Sequence 27, Appl1	1662	14.2	0.2	21	1	PCT-US96-09430-8	Sequence 8, Appl1
1590	14.2	0.2	21	1	US-08-538-816A-6	Sequence 6, Appl1	1663	14.2	0.2	21	1	PCT-US96-09430-9	Sequence 9, Appl1
1591	14.2	0.2	21	1	US-08-639-080-31	Sequence 31, Appl1	1664	14.2	0.2	21	1	PCT-US96-09430-11	Sequence 11, Appl1
1592	14.2	0.2	21	1	US-08-440-740A-36	Sequence 36, Appl1	1665	14.2	0.2	21	1	US-09-527-345-6	Sequence 6, Appl1
1593	14.2	0.2	21	1	US-08-173-489C-115	Sequence 115, App	1666	14.2	0.2	26	1	US-09-167-511-10	Sequence 10, Appl1
1594	14.2	0.2	21	1	US-08-173-489C-117	Sequence 117, App	1667	14.2	0.2	26	1	US-09-161-932A-43	Sequence 43, Appl1
1595	14.2	0.2	21	1	US-08-173-489C-118	Sequence 118, App	1668	14.2	0.2	28	1	US-08-858-767-14	Sequence 14, Appl1
1596	14.2	0.2	21	1	US-08-474-661-27	Sequence 27, Appl1	1669	14.2	0.2	30	1	US-08-863-028-14	Sequence 14, Appl1
1597	14.2	0.2	21	1	US-08-740-215B-3	Sequence 3, Appl1	1670	14.2	0.2	30	1	US-08-455-627-12	Sequence 12, Appl1
1598	14.2	0.2	21	1	US-09-076-651-6	Sequence 6, Appl1	1671	14.2	0.2	30	1	US-08-689-856-12	Sequence 12, Appl1
1599	14.2	0.2	21	1	US-08-344-155C-36	Sequence 36, Appl1	1672	14.2	0.2	30	1	US-08-787-321-12	Sequence 12, Appl1
1600	14.2	0.2	21	1	US-09-111-573-19	Sequence 19, Appl1	1673	14.2	0.2	30	1	US-09-723-265-4	Sequence 4, Appl1
1601	14.2	0.2	21	1	US-09-213-767-3	Sequence 3, Appl1	1674	14.2	0.2	14	1	US-08-173-489C-75	Sequence 75, Appl1
1602	14.2	0.2	21	1	US-08-611-977-27	Sequence 27, Appl1	1675	14.2	0.2	14	1	US-08-173-489C-16	Sequence 16, Appl1
1603	14.2	0.2	21	1	US-08-867-941-48	Sequence 48, Appl1	1676	14.2	0.2	14	1	US-08-832-021-16	Sequence 16, Appl1
1604	14.2	0.2	21	1	US-08-487-799-75	Sequence 75, Appl1	1677	14.2	0.2	14	1	US-08-832-021-61	Sequence 61, Appl1
1605	14.2	0.2	21	1	US-08-804-439A-31	Sequence 31, Appl1	1678	14.2	0.2	14	1	US-08-724-466B-14	Sequence 14, Appl1
1606	14.2	0.2	21	1	US-09-008-722-6	Sequence 6, Appl1	1679	14.2	0.2	14	1	US-09-019-095A-26	Sequence 26, Appl1
1607	14.2	0.2	21	1	US-08-982-845B-36	Sequence 36, Appl1	1680	14.2	0.2	14	1	US-08-882-164D-14	Sequence 14, Appl1
1608	14.2	0.2	21	1	US-08-720-229-31	Sequence 31, Appl1	1681	14.2	0.2	14	1	US-09-462-565B-1	Sequence 1, Appl1
1609	14.2	0.2	21	1	US-08-081-180-28	Sequence 28, Appl1	1682	14.2	0.2	14	1	US-09-619-103-20	Sequence 20, Appl1
1610	14.2	0.2	21	1	US-09-040-786-28	Sequence 28, Appl1	1683	14.2	0.2	14	1	5453496-4	Patent No. 5453496
1611	14.2	0.2	21	1	US-08-746-111-3	Sequence 3, Appl1	1684	14.2	0.2	14	1	5453496-5	Patent No. 5453496
1612	14.2	0.2	21	1	US-08-991-525B-36	Sequence 36, Appl1	1685	14.2	0.2	15	1	US-08-452-196A-3	Sequence 3, Appl1
1613	14.2	0.2	21	1	US-09-085-759-36	Sequence 36, Appl1	1686	14.2	0.2	15	1	US-08-452-196A-4	Sequence 4, Appl1
1614	14.2	0.2	21	1	US-09-344-914-2	Sequence 2, Appl1	1687	14.2	0.2	15	1	US-08-358-995-25	Sequence 25, Appl1
1615	14.2	0.2	21	1	US-08-974-549A-514	Sequence 514, App	1688	14.2	0.2	15	1	US-08-292-620A-363	Sequence 363, App
1616	14.2	0.2	21	1	US-09-128-496-36	Sequence 36, Appl1	1689	14.2	0.2	15	1	US-08-292-620A-363	Sequence 363, App
1617	14.2	0.2	21	1	US-09-235-614-31	Sequence 31, Appl1	1690	14.2	0.2	15	1	US-08-832-021-61	Sequence 61, App
1618	14.2	0.2	21	1	US-09-074-658-48	Sequence 48, Appl1	1691	14.2	0.2	15	1	US-08-832-021-61	Sequence 61, Appl1
1619	14.2	0.2	21	1	US-09-045-054-34	Sequence 34, Appl1	1692	14.2	0.2	15	1	US-08-832-021-63	Sequence 63, Appl1
1620	14.2	0.2	21	1	US-08-711-417C-34	Sequence 34, Appl1	1693	14.2	0.2	15	1	US-09-071-845-363	Sequence 363, App
1621	14.2	0.2	21	1	US-08-943-731-490	Sequence 490, App	1694	14.2	0.2	15	1	US-09-071-845-363	Sequence 363, App
1622	14.2	0.2	21	1	US-09-268-319-15	Sequence 15, Appl1	1695	14.2	0.2	15	1	US-09-071-845-363	Sequence 363, App
1623	14.2	0.2	21	1	US-09-068-319-3	Sequence 3, Appl1	1696	14.2	0.2	15	1	US-09-071-845-363	Sequence 363, App
1624	14.2	0.2	21	1	US-09-109-663-49	Sequence 49, Appl1	1697	14.2	0.2	15	1	US-09-163-488-13	Sequence 13, Appl1
1625	14.2	0.2	21	1	US-09-009-490A-36	Sequence 36, Appl1	1698	14.2	0.2	15	1	US-09-475-947A-158	Sequence 158, App
1626	14.2	0.2	21	1	US-09-522-217-11	Sequence 11, Appl1	1699	14.2	0.2	15	1	US-09-475-947A-158	Sequence 158, App
1627	14.2	0.2	21	1	US-09-522-217-11	Sequence 11, Appl1	1700	14.2	0.2	17	1	PCT-US91-03680-16	Sequence 16, Appl1
1628	14.2	0.2	21	1	US-09-522-217-51	Sequence 51, Appl1	1701	14.2	0.2	17	1	US-09-554-726A-22	Sequence 22, Appl1
1629	14.2	0.2	21	1	US-09-208-394-6	Sequence 6, Appl1	1702	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1630	14.2	0.2	21	1	US-09-177-650-23	Sequence 23, Appl1	1703	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1631	14.2	0.2	21	1	US-09-328-174A-74	Sequence 74, Appl1	1704	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1632	14.2	0.2	21	1	US-08-912-951-281	Sequence 281, App	1705	14.2	0.2	17	1	US-09-554-726A-22	Sequence 22, Appl1
1633	14.2	0.2	21	1	US-09-506-286B-60	Sequence 60, Appl1	1706	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1634	14.2	0.2	21	1	US-09-559-773A-4	Sequence 4, Appl1	1707	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1635	14.2	0.2	21	1	US-09-636-382A-10	Sequence 10, Appl1	1708	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1636	14.2	0.2	21	1	US-09-422-978-6188	Sequence 6188, Ap	1709	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1637	14.2	0.2	21	1	US-09-422-978-8873	Sequence 8873, Ap	1710	14.2	0.2	17	1	US-09-866-108A-1540	Sequence 1540, Ap
1638	14.2	0.2	21	1	US-09-422-978-10601	Sequence 10601, A	1711	14.2	0.2	18	1	US-08-066-325-52	Sequence 52, Appl1
1639	14.2	0.2	21	1	US-09-422-978-10694	Sequence 10694, A	1712	14.2	0.2	18	1	US-07-938-906-8	Sequence 8, Appl1

c1713	14	0.2	18	1	US-08-450-425-2	Sequence 2, Appli	1786	14	0.2	22	1	US-08-123-449A-19	Sequence 19, Appl
c1714	14	0.2	18	1	US-08-533-358-8	Sequence 8, Appli	1787	14	0.2	22	1	US-08-458-050-19	Sequence 19, Appl
c1715	14	0.2	18	1	US-09-285-911-31	Sequence 31, Appl	1788	14	0.2	22	1	US-08-847-844A-94	Sequence 19, Appl
c1716	14	0.2	18	1	US-09-289-376-45	Sequence 45, Appl	1789	14	0.2	22	1	US-08-950-196-19	Sequence 19, Appl
c1717	14	0.2	18	1	US-08-559-205-28	Sequence 28, Appl	1790	14	0.2	22	1	US-09-720-201A-25	Sequence 25, Appl
1718	14	0.2	18	1	US-09-630-706-41	Sequence 41, Appl	c1791	14	0.2	22	1	US-08-123-449A-1	Sequence 1, Appli
1719	14	0.2	18	1	US-09-423-978-4090	Sequence 4090, Ap	c1792	14	0.2	22	1	US-08-123-449A-2	Sequence 2, Appli
c1720	14	0.2	18	1	US-09-423-978-4743	Sequence 4743, Ap	c1793	14	0.2	22	1	US-08-458-050-1	Sequence 1, Appli
1721	14	0.2	18	1	US-09-423-978-8891	Sequence 8891, Ap	c1794	14	0.2	22	1	US-08-458-050-2	Sequence 2, Appli
c1722	14	0.2	18	1	5336598-23	Patent No. 5336598	c1795	14	0.2	22	1	US-08-950-196-1	Sequence 1, Appli
c1723	14	0.2	19	1	US-07-766-751-1	Sequence 1, Appli	c1796	14	0.2	22	1	US-08-950-196-2	Sequence 2, Appli
c1724	14	0.2	19	1	US-08-423-383-24	Sequence 24, Appli	1797	14	0.2	22	1	US-09-750-401-17	Sequence 17, Appl
c1725	14	0.2	19	1	US-08-423-383-51	Sequence 51, Appl	1798	14	0.2	22	1	US-09-750-401-19	Sequence 19, Appl
c1726	14	0.2	19	1	US-08-620-457A-62	Sequence 62, Appl	c1799	14	0.2	22	1	US-08-457-273B-31	Sequence 31, Appl
c1727	14	0.2	19	1	US-08-348-572-63	Sequence 63, Appl	1800	14	0.2	23	1	US-07-869-933-7	Sequence 7, Appli
c1728	14	0.2	19	1	US-08-437-353A-24	Sequence 24, Appl	1801	14	0.2	23	1	US-09-103-663-7	Sequence 7, Appli
c1729	14	0.2	19	1	US-08-437-353A-51	Sequence 51, Appl	1802	14	0.2	24	1	US-08-014-943B-25	Sequence 25, Appl
c1730	14	0.2	19	1	US-08-468-037A-33	Sequence 33, Appl	1803	14	0.2	24	1	US-08-486-421-50	Sequence 50, Appl
c1731	14	0.2	19	1	US-08-471-973A-33	Sequence 33, Appl	1804	14	0.2	24	1	US-08-470-911-50	Sequence 50, Appl
c1732	14	0.2	19	1	US-08-466-880-28	Sequence 28, Appl	1805	14	0.2	24	1	US-08-735-381-1	Sequence 1, Appli
c1733	14	0.2	19	1	US-09-035-357-33	Sequence 33, Appl	1806	14	0.2	24	1	US-08-486-809-50	Sequence 50, Appl
c1734	14	0.2	19	1	US-09-199-859-3	Sequence 3, Appli	1807	14	0.2	24	1	US-09-183-619-7	Sequence 7, Appli
c1735	14	0.2	19	1	US-09-041-090B-63	Sequence 63, Appli	1808	14	0.2	24	1	US-09-201-674-1	Sequence 1, Appli
c1736	14	0.2	19	1	US-09-016-520-4	Sequence 4, Appli	1809	14	0.2	24	1	US-09-536-936-11	Sequence 11, Appli
c1737	14	0.2	19	1	US-09-144-611-12	Sequence 12, Appl	1810	14	0.2	24	1	US-09-025-639-4	Sequence 4, Appli
c1738	14	0.2	19	1	US-09-135-021-65	Sequence 65, Appl	1811	14	0.2	24	1	US-09-333-237-4	Sequence 4, Appli
c1739	14	0.2	19	1	US-09-130-973-4	Sequence 4, Appli	1812	14	0.2	24	1	US-09-732-067-1	Sequence 1, Appli
c1740	14	0.2	19	1	US-09-477-902-4	Sequence 4, Appli	1813	14	0.2	24	1	US-10-043-415-4	Sequence 4, Appli
c1741	14	0.2	19	1	US-09-338-907-568	Sequence 568, App	1814	14	0.2	24	1	US-09-854-317-1	Sequence 1, Appli
c1742	14	0.2	19	1	US-09-338-907-573	Sequence 573, App	c1815	14	0.2	24	1	US-09-496-632C-11	Sequence 11, Appl
c1743	14	0.2	19	1	US-09-135-020-67	Sequence 67, Appl	c1816	14	0.2	24	1	US-09-496-632C-12	Sequence 12, Appl
c1744	14	0.2	19	1	US-09-444-871-67	Sequence 67, Appl	1817	14	0.2	24	1	US-08-924-695A-22	Sequence 22, Appl
c1745	14	0.2	19	1	US-09-453-514A-12	Sequence 12, Appl	c1818	14	0.2	25	1	US-08-341-148-2	Sequence 2, Appli
c1746	14	0.2	19	1	US-09-218-207-568	Sequence 568, App	c1819	14	0.2	25	1	US-08-460-130-2	Sequence 2, Appli
c1747	14	0.2	19	1	US-09-218-207-573	Sequence 573, App	c1820	14	0.2	25	1	US-08-969-913-1	Sequence 1, Appli
c1748	14	0.2	19	1	US-09-135-202-33	Sequence 33, Appl	c1821	14	0.2	25	1	US-09-183-619-5	Sequence 5, Appli
c1749	14	0.2	19	1	US-09-597-735-67	Sequence 67, Appl	c1822	14	0.2	25	1	US-09-382-734-23	Sequence 23, Appl
c1750	14	0.2	19	1	US-09-444-235-67	Sequence 67, Appl	c1823	14	0.2	25	1	PCT-US94-14096-2	Sequence 2, Appli
c1751	14	0.2	19	1	US-09-597-732-67	Sequence 67, Appl	c1824	14	0.2	26	1	US-08-621-814A-3	Sequence 3, Appli
c1752	14	0.2	19	1	US-08-802-331-29	Sequence 29, Appl	1825	14	0.2	26	1	US-08-910-632-5	Sequence 5, Appli
c1753	14	0.2	19	1	US-09-389-283-33	Sequence 33, Appl	1826	14	0.2	26	1	US-08-805-531A-5	Sequence 5, Appli
c1754	14	0.2	19	1	US-09-423-978-9216	Sequence 9216, Ap	1827	14	0.2	26	1	US-09-569-444-5	Sequence 5, Appli
1755	14	0.2	19	1	US-09-597-731-67	Sequence 67, Appl	c1828	14	0.2	32	1	US-08-784-208-3	Sequence 3, Appli
c1756	14	0.2	19	1	US-08-442-001C-62	Sequence 62, Appl	c1829	13.8	0.2	17	1	US-08-373-124A-970	Sequence 970, App
c1757	14	0.2	19	1	US-09-370-541-4	Sequence 4, Appli	1830	13.8	0.2	17	1	US-08-373-124A-1054	Sequence 1054, Ap
c1758	14	0.2	19	1	US-09-856-747-3	Sequence 3, Appli	1831	13.8	0.2	17	1	US-08-373-124A-1967	Sequence 1967, Ap
c1759	14	0.2	20	1	US-09-560-594-59	Sequence 59, Appl	1832	13.8	0.2	17	1	US-08-373-124A-2147	Sequence 2147, Ap
1760	14	0.2	20	1	US-07-984-044A-25	Sequence 25, Appl	c1833	13.8	0.2	17	1	US-08-327-825A-6	Sequence 6, Appli
1761	14	0.2	20	1	US-08-088-658-53	Sequence 33, Appl	c1834	13.8	0.2	17	1	US-08-758-306-453	Sequence 453, App
1762	14	0.2	20	1	US-08-458-333-25	Sequence 25, Appl	1835	13.8	0.2	17	1	US-08-758-306-661	Sequence 661, App
1763	14	0.2	20	1	US-08-117-952-15	Sequence 15, Appl	c1836	13.8	0.2	17	1	US-08-435-628-970	Sequence 970, App
1764	14	0.2	20	1	US-08-471-907A-33	Sequence 33, Appl	1837	13.8	0.2	17	1	US-08-435-628-1054	Sequence 1054, App
1765	14	0.2	20	1	US-09-280-805-79	Sequence 79, Appl	1838	13.8	0.2	17	1	US-08-435-628-1967	Sequence 1967, Ap
1766	14	0.2	20	1	US-09-488-671-114	Sequence 114, App	1839	13.8	0.2	17	1	US-08-435-628-2147	Sequence 2147, Ap
c1767	14	0.2	20	1	US-09-517-584A-81	Sequence 81, Appl	c1840	13.8	0.2	17	1	US-08-173-689C-48	Sequence 48, Appl
c1768	14	0.2	20	1	US-09-844-634-64	Sequence 64, Appl	1841	13.8	0.2	17	1	US-08-438-864-20	Sequence 20, Appl
1769	14	0.2	20	1	US-09-470-062-4	Sequence 64, Appl	c1842	13.8	0.2	17	1	US-08-531-137B-6	Sequence 6, Appli
c1770	14	0.2	20	1	US-09-851-062-4	Sequence 64, Appl	1843	13.8	0.2	17	1	US-08-988-162-434	Sequence 434, App
c1771	14	0.2	20	1	US-08-275-951-46	Sequence 46, Appl	1844	13.8	0.2	17	1	US-08-988-706-24	Sequence 24, Appl
1772	14	0.2	20	1	US-09-422-978-6254	Sequence 6254, Ap	1845	13.8	0.2	17	1	US-08-913-633-56	Sequence 56, Appl
1773	14	0.2	20	1	US-09-422-978-7396	Sequence 7396, Ap	1846	13.8	0.2	17	1	US-08-628-247-20	Sequence 20, Appl
c1774	14	0.2	20	1	US-09-198-452A-3923	Sequence 3923, Ap	1847	13.8	0.2	17	1	US-08-402-253-20	Sequence 20, Appl
c1775	14	0.2	20	1	US-09-198-452A-6060	Sequence 6060, Ap	c1848	13.8	0.2	17	1	US-09-158-765-6	Sequence 6, Appli
c1776	14	0.2	20	1	US-09-860-473-70	Sequence 70, Appli	1849	13.8	0.2	17	1	US-09-021-701-128	Sequence 128, App
1777	14	0.2	20	1	US-08-750-047-5	Sequence 5, Appli	1850	13.8	0.2	17	1	US-09-021-701-129	Sequence 129, App
c1778	14	0.2	21	1	US-08-403-888A-146	Sequence 146, App	1851	13.8	0.2	17	1	US-08-443-666B-20	Sequence 20, Appl
c1779	14	0.2	21	1	US-08-711-417C-167	Sequence 167, App	1852	13.8	0.2	17	1	US-09-580-794C-36	Sequence 36, Appl
c1780	14	0.2	21	1	US-09-422-978-9246	Sequence 9246, App	1853	13.8	0.2	17	1	US-08-584-040-2073	Sequence 2073, App
c1781	14	0.2	21	1	US-09-422-978-11157	Sequence 11157, A	c1854	13.8	0.2	17	1	US-08-584-040-2102	Sequence 2102, App
c1782	14	0.2	21	1	US-09-083-852A-9	Sequence 9, Appli	c1855	13.8	0.2	17	1	US-08-584-040-2133	Sequence 2133, App
1783	14	0.2	21	1	US-09-723-909-167	Sequence 167, App	1857	13.8	0.2	17	1	US-08-584-040-2742	Sequence 2742, Ap
c1784	14	0.2	21	1	US-09-927-842-30	Sequence 30, Appl	c1858	13.8	0.2	17	1	US-08-584-040-3895	Sequence 3895, Ap

1859	13.8	0.2	17	1	US-08-584-040-4028	Sequence 4028, Ap	c1932	13.8	0.2	18	1	US-08-483-522-6	Sequence 6, Appl1
c1860	13.8	0.2	17	1	US-08-584-040-5492	Sequence 5492, Ap	c1933	13.8	0.2	18	1	US-08-126-593A-9	Sequence 9, Appl1
1861	13.8	0.2	17	1	US-08-584-040-5832	Sequence 5832, Ap	c1934	13.8	0.2	18	1	US-08-411-796-263	Sequence 263, App
1862	13.8	0.2	17	1	US-08-584-040-7818	Sequence 7818, Ap	c1935	13.8	0.2	18	1	US-08-363-240A-1122	Sequence 1122, Ap
1863	13.8	0.2	17	1	US-08-584-040-7819	Sequence 7819, Ap	c1936	13.8	0.2	18	1	US-08-488-470A-15	Sequence 15, Appl1
1864	13.8	0.2	17	1	US-08-584-040-7820	Sequence 7820, Ap	c1937	13.8	0.2	18	1	US-08-409-902-1	Sequence 1, Appl1
1865	13.8	0.2	17	1	US-08-584-040-7821	Sequence 7821, Ap	c1938	13.8	0.2	18	1	US-08-454-039A-9	Sequence 9, Appl1
1866	13.8	0.2	17	1	US-08-584-040-7823	Sequence 7823, Ap	c1939	13.8	0.2	18	1	US-07-946-239-6	Sequence 6, Appl1
1867	13.8	0.2	17	1	US-08-584-040-8030	Sequence 8030, Ap	c1940	13.8	0.2	18	1	US-08-484-505A-15	Sequence 15, Appl1
c1868	13.8	0.2	17	1	US-08-679-645-61	Sequence 61, Appl1	c1941	13.8	0.2	18	1	US-08-367-066-11	Sequence 11, Appl1
1869	13.8	0.2	17	1	US-09-531-000-6	Sequence 6, Appl1	c1942	13.8	0.2	18	1	US-08-384-324-4	Sequence 4, Appl1
1870	13.8	0.2	17	1	US-09-474-432B-558	Sequence 558, App	c1943	13.8	0.2	18	1	US-08-585-684B-2587	Sequence 2587, Ap
1871	13.8	0.2	17	1	US-09-474-432B-657	Sequence 657, App	c1944	13.8	0.2	18	1	US-08-585-684B-2635	Sequence 2635, Ap
1872	13.8	0.2	17	1	US-09-474-432B-667	Sequence 667, App	c1945	13.8	0.2	18	1	US-08-585-684B-2687	Sequence 2687, Ap
c1873	13.8	0.2	17	1	US-09-371-772B-618	Sequence 618, App	c1946	13.8	0.2	18	1	US-08-460-751-15	Sequence 15, Appl1
c1874	13.8	0.2	17	1	US-09-371-772B-647	Sequence 647, App	c1947	13.8	0.2	18	1	US-08-951-646-14	Sequence 14, Appl1
c1875	13.8	0.2	17	1	US-09-371-772B-738	Sequence 738, App	c1948	13.8	0.2	18	1	US-08-867-941-37	Sequence 37, Appl1
1876	13.8	0.2	17	1	US-09-371-772B-1266	Sequence 1266, Ap	c1949	13.8	0.2	18	1	US-09-205-860-10	Sequence 10, Appl1
c1877	13.8	0.2	17	1	US-09-371-772B-1662	Sequence 1662, Ap	c1950	13.8	0.2	18	1	US-08-857-946-8	Sequence 8, Appl1
1878	13.8	0.2	17	1	US-09-371-772B-1795	Sequence 1795, Ap	c1951	13.8	0.2	18	1	US-08-857-946-14	Sequence 14, Appl1
c1879	13.8	0.2	17	1	US-09-371-772B-2383	Sequence 2383, Ap	c1952	13.8	0.2	18	1	US-09-256-496-64	Sequence 64, Appl1
1880	13.8	0.2	17	1	US-09-371-772B-2692	Sequence 2692, Ap	c1953	13.8	0.2	18	1	US-09-256-496-72	Sequence 72, Appl1
1881	13.8	0.2	17	1	US-09-371-772B-3602	Sequence 3602, Ap	c1954	13.8	0.2	18	1	US-09-156-253-8	Sequence 8, Appl1
1882	13.8	0.2	17	1	US-09-371-772B-3603	Sequence 3603, Ap	c1955	13.8	0.2	18	1	US-09-138-024-5	Sequence 5, Appl1
1883	13.8	0.2	17	1	US-09-371-772B-3604	Sequence 3604, Ap	c1956	13.8	0.2	18	1	US-09-205-921-40	Sequence 40, Appl1
1884	13.8	0.2	17	1	US-09-371-772B-3605	Sequence 3605, Ap	c1957	13.8	0.2	18	1	US-08-970-740-8	Sequence 8, Appl1
1885	13.8	0.2	17	1	US-09-371-772B-3607	Sequence 3607, Ap	c1958	13.8	0.2	18	1	US-08-471-039-263	Sequence 263, App
1886	13.8	0.2	17	1	US-09-371-772B-3813	Sequence 3813, Ap	c1959	13.8	0.2	18	1	US-09-358-381-32	Sequence 32, Appl1
c1887	13.8	0.2	17	1	US-09-371-772B-4950	Sequence 4950, Ap	c1960	13.8	0.2	18	1	US-09-339-964-11	Sequence 11, Appl1
c1889	13.8	0.2	17	1	US-09-371-772B-5350	Sequence 5350, Ap	c1961	13.8	0.2	18	1	US-09-029-045-9	Sequence 9, Appl1
c1890	13.8	0.2	17	1	US-09-371-772B-5639	Sequence 5639, Ap	c1962	13.8	0.2	18	1	US-09-174-437-14	Sequence 14, Appl1
c1891	13.8	0.2	17	1	US-09-371-772B-6942	Sequence 6942, Ap	c1963	13.8	0.2	18	1	US-09-151-467-6	Sequence 6, Appl1
1892	13.8	0.2	17	1	US-09-796-071-6	Sequence 6, Appl1	c1965	13.8	0.2	18	1	US-09-036-599-11	Sequence 11, Appl1
1893	13.8	0.2	17	1	US-09-476-387-557	Sequence 557, App	c1966	13.8	0.2	18	1	US-09-078-402A-15	Sequence 15, Appl1
1894	13.8	0.2	17	1	US-09-476-387-666	Sequence 666, App	c1967	13.8	0.2	18	1	US-09-074-658-37	Sequence 37, Appl1
1895	13.8	0.2	17	1	US-09-401-063-434	Sequence 434, App	c1968	13.8	0.2	18	1	US-09-038-072-2635	Sequence 2635, Ap
c1896	13.8	0.2	17	1	US-09-827-998-484	Sequence 484, App	c1970	13.8	0.2	18	1	US-09-038-072-2687	Sequence 2687, Ap
1897	13.8	0.2	17	1	US-09-829-812A-3	Sequence 3, Appl1	c1971	13.8	0.2	18	1	US-09-071-433-20	Sequence 20, Appl1
1898	13.8	0.2	17	1	US-09-866-108A-553	Sequence 553, App	c1972	13.8	0.2	18	1	US-09-475-316A-122	Sequence 122, App
1899	13.8	0.2	17	1	US-09-866-108A-554	Sequence 554, App	c1973	13.8	0.2	18	1	US-09-311-260-119	Sequence 119, App
c1901	13.8	0.2	17	1	US-09-866-108A-1127	Sequence 1127, Ap	c1974	13.8	0.2	18	1	US-09-593-322-34	Sequence 34, Appl1
c1902	13.8	0.2	17	1	US-09-866-108A-1239	Sequence 1239, Ap	c1975	13.8	0.2	18	1	US-09-251-645-7	Sequence 7, Appl1
c1903	13.8	0.2	17	1	US-09-866-108A-1842	Sequence 1842, Ap	c1976	13.8	0.2	18	1	US-09-594-108-34	Sequence 34, Appl1
1904	13.8	0.2	17	1	US-09-866-108A-1947	Sequence 1947, Ap	c1977	13.8	0.2	18	1	US-09-577-902-32	Sequence 32, Appl1
1905	13.8	0.2	17	1	US-09-866-108A-2213	Sequence 2213, Ap	c1978	13.8	0.2	18	1	US-09-344-306-34	Sequence 34, Appl1
c1906	13.8	0.2	17	1	US-09-866-108A-2214	Sequence 2214, Ap	c1979	13.8	0.2	18	1	US-08-584-040-8406	Sequence 8406, Ap
1907	13.8	0.2	17	1	US-09-866-108A-2742	Sequence 2742, Ap	c1980	13.8	0.2	18	1	US-08-584-040-8406	Sequence 8406, Ap
c1908	13.8	0.2	17	1	US-09-866-108A-5951	Sequence 5951, Ap	c1981	13.8	0.2	18	1	US-08-584-040-8414	Sequence 8414, Ap
1909	13.8	0.2	17	1	US-09-866-108A-6539	Sequence 6539, Ap	c1982	13.8	0.2	18	1	US-08-686-179A-2	Sequence 2, Appl1
c1910	13.8	0.2	17	1	US-09-866-108A-6569	Sequence 6569, Ap	c1983	13.8	0.2	18	1	US-08-679-645-575	Sequence 575, App
1911	13.8	0.2	17	1	US-09-866-108A-6859	Sequence 6859, Ap	c1984	13.8	0.2	18	1	US-08-679-645-1165	Sequence 1165, Ap
c1912	13.8	0.2	17	1	US-09-866-108A-7069	Sequence 7069, Ap	c1985	13.8	0.2	18	1	US-08-679-645-1185	Sequence 1185, Ap
c1913	13.8	0.2	17	1	US-09-866-108A-7071	Sequence 7071, Ap	c1987	13.8	0.2	18	1	US-09-404-065-10	Sequence 10, Appl1
1914	13.8	0.2	17	1	US-09-866-108A-7590	Sequence 7590, Ap	c1988	13.8	0.2	18	1	US-09-167-109-1177	Sequence 177, App
c1915	13.8	0.2	17	1	US-09-866-108A-7758	Sequence 7758, Ap	c1989	13.8	0.2	18	1	US-09-256-838-6	Sequence 6, Appl1
1917	13.8	0.2	17	1	US-09-866-108A-7801	Sequence 7801, Ap	c1990	13.8	0.2	18	1	US-09-144-367-36	Sequence 36, Appl1
1918	13.8	0.2	17	1	US-09-866-108A-7802	Sequence 7802, Ap	c1991	13.8	0.2	18	1	US-09-250-609-56	Sequence 56, Appl1
1919	13.8	0.2	17	1	US-09-866-108A-8361	Sequence 8361, Ap	c1992	13.8	0.2	18	1	US-08-559-320-263	Sequence 263, App
c1920	13.8	0.2	17	1	US-09-866-108A-8451	Sequence 8451, Ap	c1993	13.8	0.2	18	1	US-09-435-321-9	Sequence 9, Appl1
1921	13.8	0.2	17	1	US-09-866-108A-9012	Sequence 9012, Ap	c1994	13.8	0.2	18	1	US-09-555-313B-13	Sequence 13, Appl1
1922	13.8	0.2	17	1	US-09-866-108A-9013	Sequence 9013, Ap	c1995	13.8	0.2	18	1	US-09-280-030-42	Sequence 42, Appl1
1923	13.8	0.2	17	1	US-09-866-108A-9014	Sequence 9014, Ap	c1996	13.8	0.2	18	1	US-09-250-611-56	Sequence 56, Appl1
1924	13.8	0.2	17	1	US-09-866-108A-9015	Sequence 9015, Ap	c1997	13.8	0.2	18	1	US-09-573-322-5	Sequence 5, Appl1
1925	13.8	0.2	17	1	US-09-866-108A-9016	Sequence 9016, Ap	c1998	13.8	0.2	18	1	US-09-478-189-28	Sequence 28, Appl1
1926	13.8	0.2	17	1	US-09-866-108A-9254	Sequence 9254, Ap	c1999	13.8	0.2	18	1	US-09-422-978-5122	Sequence 5122, Ap
c1927	13.8	0.2	17	1	US-09-866-108A-9255	Sequence 9255, Ap	2000	13.8	0.2	18	1	US-09-422-978-7190	Sequence 7190, Ap
1928	13.8	0.2	17	1	US-09-866-108A-9530	Sequence 9530, Ap	2001	13.8	0.2	18	1	US-09-422-978-7310	Sequence 7310, Ap
1929	13.8	0.2	18	1	US-08-487-046-5	Sequence 5, Appl1	2002	13.8	0.2	18	1	US-09-422-978-8353	Sequence 8353, Ap
c1930	13.8	0.2	18	1	US-08-487-046-6	Sequence 6, Appl1	2003	13.8	0.2	18	1	US-09-422-978-10109	Sequence 10109, A
1931	13.8	0.2	18	1	US-08-483-522-5	Sequence 5, Appl1	2004	13.8	0.2	18	1	US-09-422-978-10316	Sequence 10316, A

C2005	13.8	0.2	18	1	US-09-422-978-10643	Sequence 10643, A
C2006	13.8	0.2	18	1	US-09-422-978-11081	Sequence 11081, A
C2007	13.8	0.2	18	1	US-09-422-978-11214	Sequence 11214, A
C2008	13.8	0.2	18	1	US-09-230-652-89	Sequence 89, Appl
C2009	13.8	0.2	18	1	US-09-744-154-9	Sequence 9, Appl
C2010	13.8	0.2	18	1	US-09-686-055A-14	Sequence 14, Appl
C2011	13.8	0.2	18	1	US-09-371-772B-1474	Sequence 1474, Ap
C2012	13.8	0.2	18	1	US-09-371-772B-4062	Sequence 4062, Ap
C2013	13.8	0.2	18	1	US-09-371-772B-4070	Sequence 4070, Ap
C2014	13.8	0.2	18	1	US-09-679-238A-30	Sequence 30, Appl
C2015	13.8	0.2	18	1	US-09-331-568A-8	Sequence 8, Appl
C2016	13.8	0.2	18	1	US-09-981-621-2	Sequence 2, Appl
C2017	13.8	0.2	18	1	US-09-704-640-122	Sequence 122, App
C2018	13.8	0.2	18	1	US-09-495-714C-96	Sequence 96, Appl
C2019	13.8	0.2	18	1	PCT-US92-07815-6	Sequence 263, App
C2020	13.8	0.2	18	1	PCT-US93-11198-263	Sequence 4, Appl
C2021	13.8	0.2	18	1	PCT-US96-01473-4	Sequence 9, Appl
C2022	13.8	0.2	19	1	US-07-985-691-9	Sequence 316, App
C2023	13.8	0.2	19	1	US-08-117-952-316	Sequence 4, Appl
C2024	13.8	0.2	19	1	US-08-987-418A-4	Sequence 7, Appl
C2025	13.8	0.2	19	1	US-09-371-710-7	Sequence 4, Appl
C2026	13.8	0.2	19	1	US-09-343-062-4	Sequence 7, Appl
C2027	13.8	0.2	19	1	US-09-648-386-7	Sequence 4, Appl
C2028	13.8	0.2	19	1	US-09-446-765-1	Sequence 1, Appl
C2029	13.8	0.2	19	1	US-09-564-805-54	Sequence 54, Appl
C2030	13.8	0.2	19	1	US-08-604-986-10	Sequence 10, Appl
C2031	13.8	0.2	19	1	US-09-214-555B-9	Sequence 9, Appl
C2032	13.8	0.2	19	1	US-09-302-681-73	Sequence 73, Appl
C2033	13.8	0.2	19	1	US-09-402-690-15	Sequence 15, Appl
C2034	13.8	0.2	19	1	US-09-470-661A-40	Sequence 40, Appl
C2035	13.8	0.2	19	1	US-09-216-393B-257	Sequence 257, App
C2036	13.8	0.2	19	1	US-09-540-357B-11	Sequence 11, Appl
C2037	13.8	0.2	19	1	US-09-422-978-5607	Sequence 5607, Ap
C2038	13.8	0.2	19	1	US-09-422-978-7196	Sequence 7196, Ap
C2039	13.8	0.2	19	1	US-09-422-978-8453	Sequence 8453, Ap
C2040	13.8	0.2	19	1	US-09-422-978-9771	Sequence 9771, Ap
C2041	13.8	0.2	19	1	US-09-254-776B-42	Sequence 42, Appl
C2042	13.8	0.2	19	1	US-09-672-717-143	Sequence 143, App
C2043	13.8	0.2	19	1	PCT-US91-03680-3	Sequence 3, Appl
C2044	13.8	0.2	19	1	PCT-US94-06311A-21	Sequence 21, Appl
C2045	13.8	0.2	20	1	US-09-536-259-9	Sequence 9, Appl
C2046	13.8	0.2	20	1	US-08-906-156A-87	Sequence 87, Appl
C2047	13.8	0.2	20	1	US-08-031-143B-38	Sequence 38, Appl
C2048	13.8	0.2	20	1	US-08-025-038-4	Sequence 4, Appl
C2049	13.8	0.2	20	1	US-08-271-942A-105	Sequence 105, App
C2050	13.8	0.2	20	1	US-08-104-073-9	Sequence 9, Appl
C2051	13.8	0.2	20	1	US-08-290-936-11	Sequence 11, Appl
C2052	13.8	0.2	20	1	US-08-320-604A-1	Sequence 16, Appl
C2053	13.8	0.2	20	1	US-08-487-411B-16	Sequence 186, App
C2054	13.8	0.2	20	1	US-08-271-880A-188	Sequence 16, Appl
C2055	13.8	0.2	20	1	US-08-535-230A-16	Sequence 16, Appl
C2056	13.8	0.2	20	1	US-08-363-233B-4	Sequence 4, Appl
C2057	13.8	0.2	20	1	US-08-481-633B-3	Sequence 3, Appl
C2058	13.8	0.2	20	1	US-08-480-493A-3	Sequence 3, Appl
C2059	13.8	0.2	20	1	US-08-616-368A-5	Sequence 5, Appl
C2060	13.8	0.2	20	1	US-08-482-638A-3	Sequence 3, Appl
C2061	13.8	0.2	20	1	US-08-559-303B-56	Sequence 56, Appl
C2062	13.8	0.2	20	1	US-08-577-858A-26	Sequence 26, Appl
C2063	13.8	0.2	20	1	US-08-632-575B-5	Sequence 5, Appl
C2064	13.8	0.2	20	1	US-08-485-611A-5	Sequence 5, Appl
C2065	13.8	0.2	20	1	US-08-651-692-9	Sequence 9, Appl
C2066	13.8	0.2	20	1	US-08-852-807-21	Sequence 21, Appl
C2067	13.8	0.2	20	1	US-08-927-561-16	Sequence 16, Appl
C2068	13.8	0.2	20	1	US-08-713-557B-20	Sequence 20, Appl
C2069	13.8	0.2	20	1	US-08-832-658A-4	Sequence 4, Appl
C2070	13.8	0.2	20	1	US-08-912-139A-2	Sequence 2, Appl
C2071	13.8	0.2	20	1	US-08-850-993-7	Sequence 7, Appl
C2072	13.8	0.2	20	1	US-08-997-080-38	Sequence 38, Appl
C2073	13.8	0.2	20	1	US-08-910-408-188	Sequence 188, App
C2074	13.8	0.2	20	1	US-08-997-362-38	Sequence 38, Appl
C2075	13.8	0.2	20	1	US-08-962-284-12	Sequence 12, Appl
C2076	13.8	0.2	20	1	US-08-874-186-20	Sequence 20, Appl
C2077	13.8	0.2	20	1	US-08-873-970-38	Sequence 38, Appl
C2078	13.8	0.2	20	1	US-08-974-180-5	Sequence 5, Appl
C2079	13.8	0.2	20	1	US-08-911-894-75	Sequence 75, Appl
C2080	13.8	0.2	20	1	US-08-755-587-195	Sequence 195, App
C2081	13.8	0.2	20	1	US-09-357-070-23	Sequence 23, Appl
C2082	13.8	0.2	20	1	US-08-779-916A-105	Sequence 105, App
C2083	13.8	0.2	20	1	US-09-106-217-3	Sequence 3, Appl
C2084	13.8	0.2	20	1	US-09-166-186-58	Sequence 58, Appl
C2085	13.8	0.2	20	1	US-09-166-186-196	Sequence 196, App
C2086	13.8	0.2	20	1	US-09-166-186-196	Sequence 196, App
C2087	13.8	0.2	20	1	US-08-988-706-43	Sequence 43, Appl
C2088	13.8	0.2	20	1	US-09-344-914-70	Sequence 70, Appl
C2089	13.8	0.2	20	1	US-09-344-914-71	Sequence 71, Appl
C2090	13.8	0.2	20	1	US-09-418-641-80	Sequence 80, Appl
C2091	13.8	0.2	20	1	US-09-392-350-46	Sequence 46, Appl
C2092	13.8	0.2	20	1	US-09-428-584-18	Sequence 18, Appl
C2093	13.8	0.2	20	1	US-09-054-298-5	Sequence 5, Appl
C2094	13.8	0.2	20	1	US-09-286-704-33	Sequence 33, Appl
C2095	13.8	0.2	20	1	US-09-249-215-188	Sequence 188, App
C2096	13.8	0.2	20	1	US-09-095-855-38	Sequence 38, Appl
C2097	13.8	0.2	20	1	US-09-444-053-70	Sequence 70, Appl
C2098	13.8	0.2	20	1	US-09-433-699-44	Sequence 44, Appl
C2099	13.8	0.2	20	1	US-09-433-699-62	Sequence 62, Appl
C2100	13.8	0.2	20	1	US-09-433-694-25	Sequence 25, Appl
C2101	13.8	0.2	20	1	US-09-513-729B-15	Sequence 15, Appl
C2102	13.8	0.2	20	1	US-09-513-729B-87	Sequence 87, Appl
C2103	13.8	0.2	20	1	US-09-428-219-32	Sequence 32, Appl
C2104	13.8	0.2	20	1	US-09-490-692-121	Sequence 121, App
C2105	13.8	0.2	20	1	US-09-490-692-121	Sequence 121, App
C2106	13.8	0.2	20	1	US-09-488-671-140	Sequence 140, App
C2107	13.8	0.2	20	1	US-09-306-876A-5	Sequence 5, Appl
C2108	13.8	0.2	20	1	US-09-306-876A-5	Sequence 6, Appl
C2109	13.8	0.2	20	1	US-09-517-584A-57	Sequence 57, Appl
C2110	13.8	0.2	20	1	US-09-290-640-77	Sequence 77, Appl
C2111	13.8	0.2	20	1	US-09-175-828-56	Sequence 56, Appl
C2112	13.8	0.2	20	1	US-09-313-932-58	Sequence 58, Appl
C2113	13.8	0.2	20	1	US-09-313-932-196	Sequence 196, App
C2114	13.8	0.2	20	1	US-09-313-932-196	Sequence 196, App
C2115	13.8	0.2	20	1	US-09-313-932-363	Sequence 363, App
C2116	13.8	0.2	20	1	US-09-313-932-477	Sequence 477, App
C2117	13.8	0.2	20	1	US-08-928-213B-41	Sequence 41, Appl
C2118	13.8	0.2	20	1	US-09-021-701-667	Sequence 67, App
C2119	13.8	0.2	20	1	US-09-021-701-668	Sequence 68, App
C2120	13.8	0.2	20	1	US-09-021-701-1052	Sequence 1052, Ap
C2121	13.8	0.2	20	1	US-09-021-701-1053	Sequence 1053, Ap
C2122	13.8	0.2	20	1	US-09-021-701-1054	Sequence 1054, Ap
C2123	13.8	0.2	20	1	US-09-021-701-1055	Sequence 1055, Ap
C2124	13.8	0.2	20	1	US-08-818-655-5	Sequence 5, Appl
C2125	13.8	0.2	20	1	US-09-657-481A-27	Sequence 27, Appl
C2126	13.8	0.2	20	1	US-09-428-583-89	Sequence 89, Appl
C2127	13.8	0.2	20	1	US-09-593-711A-37	Sequence 37, Appl
C2128	13.8	0.2	20	1	US-08-705-347A-38	Sequence 38, Appl
C2129	13.8	0.2	20	1	US-09-284-832-20	Sequence 20, Appl
C2130	13.8	0.2	20	1	US-09-484-617-124	Sequence 24, Appl
C2131	13.8	0.2	20	1	US-09-484-617-139	Sequence 139, App
C2132	13.8	0.2	20	1	US-09-536-094-11	Sequence 11, Appl
C2133	13.8	0.2	20	1	US-09-336-447A-70	Sequence 70, Appl
C2134	13.8	0.2	20	1	US-09-336-447A-71	Sequence 71, Appl
C2135	13.8	0.2	20	1	US-09-324-542-38	Sequence 38, Appl
C2136	13.8	0.2	20	1	US-09-711-303-6	Sequence 6, Appl
C2137	13.8	0.2	20	1	US-07-711-303-13	Sequence 13, Appl
C2138	13.8	0.2	20	1	US-09-434-131A-8	Sequence 8, Appl
C2139	13.8	0.2	20	1	US-09-043-149A-17	Sequence 17, Appl
C2140	13.8	0.2	20	1	US-09-716-161A-38	Sequence 38, Appl
C2141	13.8	0.2	20	1	US-09-561-497-43	Sequence 43, Appl
C2142	13.8	0.2	20	1	US-09-651-497-66	Sequence 66, Appl
C2143	13.8	0.2	20	1	US-09-659-191A-41	Sequence 41, Appl
C2144	13.8	0.2	20	1	US-09-308-759A-30	Sequence 30, Appl
C2145	13.8	0.2	20	1	US-09-851-520-35	Sequence 35, Appl
C2146	13.8	0.2	20	1	US-09-205-426-38	Sequence 38, Appl
C2147	13.8	0.2	20	1	US-09-844-634-20	Sequence 20, Appl
C2148	13.8	0.2	20	1	US-09-851-896-33	Sequence 33, Appl
C2149	13.8	0.2	20	1	US-09-254-465A-17	Sequence 17, Appl
C2150	13.8	0.2	20	1	US-09-200-643-38	Sequence 38, Appl

C2151	13.8	0.2	20	1	US-09-689-221A-12	Sequence 12, Appl	C2224	13.8	0.2	21	1	US-08-173-489C-117	Sequence 117, Appl
C2152	13.8	0.2	20	1	US-08-744-481A-42	Sequence 42, Appl	C2225	13.8	0.2	21	1	US-09-422-978-10694	Sequence 10694, A
C2153	13.8	0.2	20	1	US-09-661-753-2	Sequence 2, Appl1	C2226	13.8	0.2	21	1	PCT-US94-06661-3	Sequence 3, Appl1
C2154	13.8	0.2	20	1	US-09-907-843-62	Sequence 62, Appl	C2227	13.8	0.2	21	1	PCT-US96-09430-9	Sequence 9, Appl1
C2155	13.8	0.2	20	1	US-09-907-843-65	Sequence 65, Appl	C2228	13.8	0.2	21	1	US-07-856-124-6	Sequence 6, Appl1
C2156	13.8	0.2	20	1	US-09-676-610B-4	Sequence 4, Appl1	C2229	13.8	0.2	21	1	US-08-071-601-12	Sequence 12, Appl
C2157	13.8	0.2	20	1	US-09-640-101-33	Sequence 33, Appl1	C2230	13.8	0.2	21	1	US-08-166-301-4	Sequence 4, Appl1
C2158	13.8	0.2	20	1	US-09-517-467B-241	Sequence 241, Appl	C2231	13.8	0.2	21	1	US-08-356-901-8	Sequence 8, Appl1
C2159	13.8	0.2	20	1	US-09-300-008B-26	Sequence 26, Appl	C2232	13.8	0.2	21	1	US-08-566-347-8	Sequence 8, Appl1
C2160	13.8	0.2	20	1	US-09-657-453A-67	Sequence 67, Appl	C2233	13.8	0.2	21	1	US-08-122-795B-9	Sequence 9, Appl1
C2161	13.8	0.2	20	1	US-09-918-686-54	Sequence 54, Appl	C2234	13.8	0.2	21	1	US-08-619-598-6	Sequence 6, Appl1
C2162	13.8	0.2	20	1	US-09-199-542B-5	Sequence 5, Appl1	C2235	13.8	0.2	21	1	US-08-588-821-16	Sequence 46, Appl
C2163	13.8	0.2	20	1	US-09-527-030G-349	Sequence 349, Appl	C2236	13.8	0.2	21	1	US-08-526-654A-119	Sequence 119, Appl
C2164	13.8	0.2	20	1	US-09-725-265-39	Sequence 39, Appl	C2237	13.8	0.2	21	1	US-08-593-855A-127	Sequence 127, Appl
C2165	13.8	0.2	20	1	US-09-659-845A-147	Sequence 147, Appl	C2238	13.8	0.2	21	1	US-08-632-835-8	Sequence 8, Appl1
C2166	13.8	0.2	20	1	US-09-657-346A-104	Sequence 104, Appl	C2239	13.8	0.2	21	1	US-08-294-424-18	Sequence 38, Appl
C2167	13.8	0.2	20	1	US-09-305-839-5	Sequence 5, Appl1	C2240	13.8	0.2	21	1	US-08-915-214-46	Sequence 46, Appl
C2168	13.8	0.2	20	1	US-09-422-978-4151	Sequence 4151, Appl	C2241	13.8	0.2	21	1	US-08-726-575A-3	Sequence 3, Appl1
C2169	13.8	0.2	20	1	US-09-422-978-5517	Sequence 5517, Appl	C2242	13.8	0.2	21	1	US-08-622-100-12	Sequence 12, Appl
C2170	13.8	0.2	20	1	US-09-422-978-6065	Sequence 6065, Appl	C2243	13.8	0.2	21	1	US-08-633-558-28	Sequence 28, Appl
C2171	13.8	0.2	20	1	US-09-422-978-6799	Sequence 6799, Appl	C2244	13.8	0.2	21	1	US-08-410-784A-7	Sequence 7, Appl1
C2172	13.8	0.2	20	1	US-09-423-978-7498	Sequence 7498, Appl	C2245	13.8	0.2	21	1	US-08-480-020B-12	Sequence 12, Appl
C2173	13.8	0.2	20	1	US-09-423-978-8813	Sequence 8813, Appl	C2246	13.8	0.2	21	1	US-08-480-020B-13	Sequence 13, Appl
C2174	13.8	0.2	20	1	US-09-060-299-61	Sequence 61, Appl	C2247	13.8	0.2	21	1	US-09-005-532-16	Sequence 46, Appl
C2175	13.8	0.2	20	1	US-09-060-299-391	Sequence 391, Appl	C2248	13.8	0.2	21	1	US-08-910-618-12	Sequence 12, Appl
C2176	13.8	0.2	20	1	US-09-705-267A-31	Sequence 31, Appl	C2249	13.8	0.2	21	1	US-08-910-618-13	Sequence 13, Appl
C2177	13.8	0.2	20	1	US-09-705-267A-34	Sequence 34, Appl	C2250	13.8	0.2	21	1	US-08-822-028-47	Sequence 47, Appl
C2178	13.8	0.2	20	1	US-09-403-923A-61	Sequence 61, Appl	C2251	13.8	0.2	21	1	US-08-822-028-48	Sequence 48, Appl
C2179	13.8	0.2	20	1	US-09-403-923A-391	Sequence 391, Appl	C2252	13.8	0.2	21	1	US-08-899-786-31	Sequence 31, Appl
C2180	13.8	0.2	20	1	US-09-198-452A-1354	Sequence 1354, Appl	C2253	13.8	0.2	21	1	US-08-445-463B-94	Sequence 94, Appl
C2181	13.8	0.2	20	1	US-09-198-452A-1518	Sequence 1518, Appl	C2254	13.8	0.2	21	1	US-08-445-463B-95	Sequence 95, Appl
C2182	13.8	0.2	20	1	US-09-198-452A-2177	Sequence 2177, Appl	C2255	13.8	0.2	21	1	US-09-106-217-10	Sequence 10, Appl
C2183	13.8	0.2	20	1	US-09-198-452A-2793	Sequence 2793, Appl	C2256	13.8	0.2	21	1	US-09-009-913-127	Sequence 127, Appl
C2184	13.8	0.2	20	1	US-09-198-452A-2814	Sequence 2814, Appl	C2257	13.8	0.2	21	1	US-08-445-464C-94	Sequence 94, Appl
C2185	13.8	0.2	20	1	US-09-198-452A-2863	Sequence 2863, Appl	C2258	13.8	0.2	21	1	US-08-445-464C-95	Sequence 95, Appl
C2186	13.8	0.2	20	1	US-09-198-452A-3031	Sequence 3031, Appl	C2259	13.8	0.2	21	1	US-08-923-329-23	Sequence 23, Appl
C2187	13.8	0.2	20	1	US-09-198-452A-3229	Sequence 3229, Appl	C2260	13.8	0.2	21	1	US-08-923-329-85	Sequence 85, Appl
C2188	13.8	0.2	20	1	US-09-198-452A-3792	Sequence 3792, Appl	C2261	13.8	0.2	21	1	US-08-905-359A-5	Sequence 5, Appl1
C2189	13.8	0.2	20	1	US-09-198-452A-3806	Sequence 3806, Appl	C2262	13.8	0.2	21	1	US-09-217-490-15	Sequence 15, Appl
C2190	13.8	0.2	20	1	US-09-198-452A-4100	Sequence 4100, Appl	C2263	13.8	0.2	21	1	US-08-974-549A-444	Sequence 444, Appl
C2191	13.8	0.2	20	1	US-09-198-452A-4101	Sequence 4101, Appl	C2264	13.8	0.2	21	1	US-09-353-556-5	Sequence 5, Appl1
C2192	13.8	0.2	20	1	US-09-198-452A-4289	Sequence 4289, Appl	C2265	13.8	0.2	21	1	US-08-478-285-45	Sequence 47, Appl
C2193	13.8	0.2	20	1	US-09-198-452A-4674	Sequence 4674, Appl	C2266	13.8	0.2	21	1	US-08-478-285-48	Sequence 48, Appl
C2194	13.8	0.2	20	1	US-09-198-452A-4963	Sequence 4963, Appl	C2267	13.8	0.2	21	1	US-08-973-124-270	Sequence 270, Appl
C2195	13.8	0.2	20	1	US-09-198-452A-5344	Sequence 5344, Appl	C2268	13.8	0.2	21	1	US-08-910-332-12	Sequence 12, Appl
C2196	13.8	0.2	20	1	US-09-198-452A-5420	Sequence 5420, Appl	C2269	13.8	0.2	21	1	US-08-910-332-13	Sequence 13, Appl
C2197	13.8	0.2	20	1	US-09-198-452A-5800	Sequence 5800, Appl	C2270	13.8	0.2	21	1	US-09-923-240-38	Sequence 28, Appl
C2198	13.8	0.2	20	1	US-09-198-452A-5852	Sequence 5852, Appl	C2271	13.8	0.2	21	1	US-08-943-731-396	Sequence 36, Appl
C2199	13.8	0.2	20	1	US-09-198-452A-5937	Sequence 5937, Appl	C2272	13.8	0.2	21	1	US-08-484-939A-12	Sequence 12, Appl
C2200	13.8	0.2	20	1	US-09-198-452A-5947	Sequence 5947, Appl	C2273	13.8	0.2	21	1	US-08-484-939A-13	Sequence 13, Appl
C2201	13.8	0.2	20	1	US-09-198-452A-6635	Sequence 6635, Appl	C2274	13.8	0.2	21	1	US-09-354-231B-21	Sequence 21, Appl
C2202	13.8	0.2	20	1	US-09-679-299A-147	Sequence 147, Appl	C2275	13.8	0.2	21	1	US-09-397-168-37	Sequence 37, Appl
C2203	13.8	0.2	20	1	US-09-081-385-82	Sequence 82, Appl	C2276	13.8	0.2	21	1	US-09-543-084A-5	Sequence 5, Appl1
C2204	13.8	0.2	20	1	US-09-081-385-85	Sequence 85, Appl	C2277	13.8	0.2	21	1	US-09-495-797-7	Sequence 7, Appl1
C2205	13.8	0.2	20	1	US-09-081-385-103	Sequence 103, Appl	C2278	13.8	0.2	21	1	US-09-593-012-17	Sequence 17, Appl
C2206	13.8	0.2	20	1	US-09-780-045-125	Sequence 125, Appl	C2279	13.8	0.2	21	1	US-09-593-012-26	Sequence 26, Appl
C2207	13.8	0.2	20	1	US-09-689-065B-11	Sequence 11, Appl	C2280	13.8	0.2	21	1	US-09-593-012-32	Sequence 32, Appl
C2208	13.8	0.2	20	1	US-09-112-580-102	Sequence 102, Appl	C2281	13.8	0.2	21	1	US-09-593-012-41	Sequence 41, Appl
C2209	13.8	0.2	20	1	US-09-526-193A-105	Sequence 105, Appl	C2282	13.8	0.2	21	1	US-09-099-053-24	Sequence 24, Appl
C2210	13.8	0.2	20	1	US-09-989-002-7	Sequence 7, Appl1	C2283	13.8	0.2	21	1	US-08-936-107A-26	Sequence 26, Appl
C2211	13.8	0.2	20	1	US-09-907-794A-125	Sequence 125, Appl	C2284	13.8	0.2	21	1	US-09-128-602B-21	Sequence 21, Appl
C2212	13.8	0.2	20	1	US-09-665-615B-77	Sequence 77, Appl	C2285	13.8	0.2	21	1	US-08-044-857D-94	Sequence 94, Appl
C2213	13.8	0.2	20	1	US-09-860-473-76	Sequence 76, Appl	C2286	13.8	0.2	21	1	US-08-044-857D-95	Sequence 95, Appl
C2214	13.8	0.2	20	1	US-09-905-125A-125	Sequence 125, Appl	C2287	13.8	0.2	21	1	US-08-912-951-211	Sequence 211, Appl
C2215	13.8	0.2	20	1	US-09-980-052-63	Sequence 63, Appl	C2288	13.8	0.2	21	1	US-08-912-951-212	Sequence 212, Appl
C2216	13.8	0.2	20	1	US-09-902-775A-125	Sequence 125, Appl	C2289	13.8	0.2	21	1	US-09-470-661A-15	Sequence 15, Appl
C2217	13.8	0.2	20	1	PCT-US94-02891-38	Sequence 38, Appl	C2290	13.8	0.2	21	1	US-09-384-472-13	Sequence 12, Appl
C2218	13.8	0.2	20	1	PCT-US94-06331A-60	Sequence 60, Appl	C2291	13.8	0.2	21	1	US-09-384-472-13	Sequence 13, Appl
C2219	13.8	0.2	20	1	PCT-US95-08604-105	Sequence 105, Appl	C2292	13.8	0.2	21	1	US-09-422-978-7896	Sequence 7896, Appl
C2220	13.8	0.2	20	1	PCT-US96-09388-16	Sequence 16, Appl	C2293	13.8	0.2	21	1	US-09-422-978-8974	Sequence 8974, Appl
C2221	13.8	0.2	20	1	5219727-9	Sequence 15, Appl	C2294	13.8	0.2	21	1	US-09-422-978-9102	Sequence 9102, Appl
C2222	13.8	0.2	20	1	US-09-422-978-9563	Sequence 9563, Appl	C2295	13.8	0.2	21	1	US-09-422-978-9319	Sequence 9319, Appl
C2223	13.8	0.2	21	1	US-08-076-090-3	Sequence 3, Appl1	C2296	13.8	0.2	21	1	US-09-422-978-11523	Sequence 11523, A

C2297	13.8	0.2	21	1	US-09-422-978-11631	Sequence 11631, A	C2370	13.6	0.2	20	1	US-08-384-490-7	Sequence 7, Appl
C2298	13.8	0.2	21	1	US-09-460-548B-15	Sequence 15, Appl	C2371	13.6	0.2	20	1	US-08-106-802-13	Sequence 13, Appl
C2299	13.8	0.2	21	1	US-09-402-181B-444	Sequence 444, App	C2372	13.6	0.2	20	1	US-08-379-078-33	Sequence 33, App
C2300	13.8	0.2	21	1	US-09-721-456-444	Sequence 444, App	C2373	13.6	0.2	20	1	US-08-502-185-13	Sequence 13, Appl
C2301	13.8	0.2	21	1	US-09-674-826B-11	Sequence 11, Appl	C2374	13.6	0.2	20	1	US-08-502-185-25	Sequence 25, Appl
C2302	13.8	0.2	21	1	US-09-503-653A-47	Sequence 47, Appl	C2375	13.6	0.2	20	1	US-08-398-945-13	Sequence 13, Appl
C2303	13.8	0.2	21	1	US-09-503-653A-48	Sequence 48, Appl	C2376	13.6	0.2	20	1	US-08-398-945-25	Sequence 25, Appl
C2304	13.8	0.2	21	1	US-09-995-297-21	Sequence 21, Appl	C2377	13.6	0.2	20	1	US-08-233-009-17	Sequence 17, Appl
C2305	13.8	0.2	21	1	US-09-382-552-221	Sequence 221, App	C2378	13.6	0.2	20	1	US-08-261-822A-55	Sequence 55, Appl
C2306	13.8	0.2	21	1	PCT-US94-03437-94	Sequence 94, Appl	C2379	13.6	0.2	20	1	US-08-484-138-36	Sequence 13, Appl
C2307	13.8	0.2	21	1	PCT-US94-03437-95	Sequence 95, Appl	C2380	13.6	0.2	20	1	US-08-501-779-13	Sequence 13, Appl
C2308	13.8	0.2	21	1	PCT-US94-09963A-9	Sequence 9, Appl	C2381	13.6	0.2	20	1	US-08-501-779-25	Sequence 25, Appl
C2309	13.8	0.2	21	1	PCT-US96-08014-270	Sequence 270, App	C2382	13.6	0.2	20	1	US-08-195-152-8	Sequence 8, Appl
C2310	13.8	0.2	24	1	US-08-200-807-3	Sequence 3, Appl	C2383	13.6	0.2	20	1	US-08-363-585-38	Sequence 38, Appl
C2311	13.8	0.2	29	1	US-08-488-305A-3	Sequence 5, Appl	C2384	13.6	0.2	20	1	US-08-363-585-40	Sequence 40, Appl
C2312	13.8	0.2	29	1	US-08-227-476-5	Sequence 5, Appl	C2385	13.6	0.2	20	1	US-08-363-585-42	Sequence 42, Appl
C2313	13.8	0.2	30	1	US-08-480-784-41	Sequence 41, Appl	C2386	13.6	0.2	20	1	US-08-363-585-44	Sequence 44, Appl
C2314	13.8	0.2	30	1	US-08-483-553-41	Sequence 41, Appl	C2387	13.6	0.2	20	1	US-08-363-585-46	Sequence 46, Appl
C2315	13.8	0.2	30	1	US-08-487-002-41	Sequence 41, Appl	C2388	13.6	0.2	20	1	US-08-356-287-23	Sequence 23, Appl
C2316	13.8	0.2	30	1	US-08-483-554B-41	Sequence 41, Appl	C2389	13.6	0.2	20	1	US-08-413-118-28	Sequence 28, Appl
C2317	13.8	0.2	30	1	US-08-488-011B-41	Sequence 41, Appl	C2390	13.6	0.2	20	1	US-08-271-880A-172	Sequence 172, App
C2318	13.8	0.2	30	1	US-08-850-727-41	Sequence 41, Appl	C2391	13.6	0.2	20	1	US-08-271-880B-189	Sequence 189, App
C2319	13.8	0.2	30	1	PCT-US95-10202-41	Sequence 41, Appl	C2392	13.6	0.2	20	1	US-08-535-230A-4	Sequence 4, Appl
C2320	13.8	0.2	30	1	PCT-US95-10203-41	Sequence 41, Appl	C2393	13.6	0.2	20	1	US-08-501-713-13	Sequence 13, Appl
C2321	13.8	0.2	33	1	PCT-US95-10220-41	Sequence 41, Appl	C2394	13.6	0.2	20	1	US-08-501-713-25	Sequence 25, Appl
C2322	13.8	0.2	33	1	US-08-465-384-4	Sequence 4, Appl	C2395	13.6	0.2	20	1	US-08-117-083-2	Sequence 2, Appl
C2323	13.6	0.2	20	1	US-08-146-504-16	Sequence 16, Appl	C2396	13.6	0.2	20	1	US-08-378-660-13	Sequence 13, Appl
C2324	13.6	0.2	20	1	US-08-379-593-5	Sequence 5, Appl	C2397	13.6	0.2	20	1	US-08-378-660-25	Sequence 25, Appl
C2325	13.6	0.2	20	1	US-08-725-976-16	Sequence 16, Appl	C2398	13.6	0.2	20	1	US-08-689-936-8	Sequence 8, Appl
C2326	13.6	0.2	20	1	US-08-997-080-83	Sequence 83, Appl	C2399	13.6	0.2	20	1	US-08-459-883-7	Sequence 7, Appl
C2327	13.6	0.2	20	1	US-08-997-362-83	Sequence 83, Appl	C2400	13.6	0.2	20	1	US-08-224-391-5	Sequence 5, Appl
C2328	13.6	0.2	20	1	US-08-965-780-1	Sequence 83, Appl	C2401	13.6	0.2	20	1	US-08-484-304-5	Sequence 5, Appl
C2329	13.6	0.2	20	1	US-08-873-970-83	Sequence 83, Appl	C2402	13.6	0.2	20	1	US-08-689-935-8	Sequence 8, Appl
C2330	13.6	0.2	20	1	US-08-765-340-96	Sequence 96, Appl	C2403	13.6	0.2	20	1	US-08-224-657-5	Sequence 5, Appl
C2331	13.6	0.2	20	1	US-09-095-855-83	Sequence 83, Appl	C2404	13.6	0.2	20	1	US-08-692-725-8	Sequence 8, Appl
C2332	13.6	0.2	20	1	US-09-407-675-1	Sequence 1, Appl	C2405	13.6	0.2	20	1	US-08-475-063-5	Sequence 5, Appl
C2333	13.6	0.2	20	1	US-09-250-075-1	Sequence 1, Appl	C2406	13.6	0.2	20	1	US-08-307-792-5	Sequence 5, Appl
C2334	13.6	0.2	20	1	US-09-173-936B-14	Sequence 14, Appl	C2407	13.6	0.2	20	1	US-08-487-412-21	Sequence 21, Appl
C2335	13.6	0.2	20	1	US-09-454-704A-13	Sequence 13, Appl	C2408	13.6	0.2	20	1	US-08-709-409-5	Sequence 5, Appl
C2336	13.6	0.2	20	1	US-09-324-542-83	Sequence 83, Appl	C2409	13.6	0.2	20	1	US-08-257-073-1	Sequence 1, Appl
C2337	13.6	0.2	20	1	US-09-205-426-83	Sequence 83, Appl	C2410	13.6	0.2	20	1	US-08-303-875-5	Sequence 5, Appl
C2338	13.6	0.2	20	1	US-09-619-103-26	Sequence 26, Appl	C2411	13.6	0.2	20	1	US-08-458-101-5	Sequence 5, Appl
C2339	13.6	0.2	20	1	US-09-726-096A-1	Sequence 1, Appl	C2412	13.6	0.2	20	1	US-08-753-147-70	Sequence 70, Appl
C2340	13.6	0.2	20	1	US-09-603-830-55	Sequence 55, Appl	C2413	13.6	0.2	20	1	US-08-531-556-116	Sequence 116, App
C2341	13.6	0.2	20	1	US-09-976-978A-55	Sequence 55, Appl	C2414	13.6	0.2	20	1	US-08-371-001-10	Sequence 10, Appl
C2342	13.6	0.2	20	1	US-09-344-260A-10	Sequence 10, Appl	C2415	13.6	0.2	20	1	US-08-640-672-8	Sequence 8, Appl
C2343	13.6	0.2	20	1	US-09-961-949A-55	Sequence 55, Appl	C2416	13.6	0.2	20	1	US-08-729-447-7	Sequence 7, Appl
C2344	13.6	0.2	20	1	US-09-966-491A-55	Sequence 55, Appl	C2417	13.6	0.2	20	1	US-08-110-691A-35	Sequence 35, Appl
C2345	13.6	0.2	20	1	US-09-957-313A-55	Sequence 55, Appl	C2418	13.6	0.2	20	1	US-08-143-881A-9	Sequence 9, Appl
C2346	13.6	0.2	20	1	US-09-966-312-55	Sequence 55, Appl	C2419	13.6	0.2	20	1	US-08-501-626-13	Sequence 13, Appl
C2347	13.6	0.2	20	1	US-09-975-062A-55	Sequence 55, Appl	C2420	13.6	0.2	20	1	US-08-501-626-25	Sequence 25, Appl
C2348	13.6	0.2	20	1	US-09-976-971A-55	Sequence 55, Appl	C2421	13.6	0.2	20	1	US-08-410-779B-60	Sequence 60, Appl
C2349	13.6	0.2	20	1	PCT-US93-07603-6	Sequence 6, Appl	C2422	13.6	0.2	20	1	US-08-501-356-13	Sequence 13, Appl
C2350	13.6	0.2	20	1	US-09-808-358-18	Sequence 18, Appl	C2423	13.6	0.2	20	1	US-08-501-356-25	Sequence 25, Appl
C2351	13.6	0.2	20	1	US-09-808-358-44	Sequence 44, Appl	C2424	13.6	0.2	20	1	US-08-560-231-17	Sequence 17, Appl
C2352	13.6	0.2	20	1	US-07-752-101A-27	Sequence 27, Appl	C2425	13.6	0.2	20	1	US-08-688-088-5	Sequence 5, Appl
C2353	13.6	0.2	20	1	US-08-036-217-5	Sequence 5, Appl	C2426	13.6	0.2	20	1	US-08-684-498A-8	Sequence 8, Appl
C2354	13.6	0.2	20	1	US-07-641-143B-3	Sequence 3, Appl	C2427	13.6	0.2	20	1	US-08-184-009-5	Sequence 5, Appl
C2355	13.6	0.2	20	1	US-08-004-552-1	Sequence 1, Appl	C2428	13.6	0.2	20	1	US-08-577-858A-8	Sequence 8, Appl
C2356	13.6	0.2	20	1	US-08-105-483-5	Sequence 5, Appl	C2429	13.6	0.2	20	1	US-08-790-963-5	Sequence 50, Appl
C2357	13.6	0.2	20	1	US-08-073-962-21	Sequence 21, Appl	C2430	13.6	0.2	20	1	US-08-753-879A-12	Sequence 12, Appl
C2358	13.6	0.2	20	1	US-07-714-687-5	Sequence 5, Appl	C2431	13.6	0.2	20	1	US-08-486-869-5	Sequence 5, Appl
C2359	13.6	0.2	20	1	US-08-150-531-26	Sequence 26, Appl	C2432	13.6	0.2	20	1	US-08-692-726-8	Sequence 8, Appl
C2360	13.6	0.2	20	1	US-08-220-151-28	Sequence 28, Appl	C2433	13.6	0.2	20	1	US-08-117-952-317	Sequence 317, App
C2361	13.6	0.2	20	1	US-08-281-082A-2	Sequence 2, Appl	C2434	13.6	0.2	20	1	US-08-578-551-26	Sequence 26, Appl
C2362	13.6	0.2	20	1	US-08-242-664-36	Sequence 36, Appl	C2435	13.6	0.2	20	1	US-08-887-365-29	Sequence 29, Appl
C2363	13.6	0.2	20	1	US-07-665-960A-13	Sequence 13, Appl	C2436	13.6	0.2	20	1	US-08-468-037A-17	Sequence 17, Appl
C2364	13.6	0.2	20	1	US-07-955-718-9	Sequence 9, Appl	C2437	13.6	0.2	20	1	US-08-626-169-19	Sequence 19, Appl
C2365	13.6	0.2	20	1	US-07-955-718-11	Sequence 11, Appl	C2438	13.6	0.2	20	1	US-08-417-210A-5	Sequence 5, Appl
C2366	13.6	0.2	20	1	US-08-379-081B-353	Sequence 353, App	C2439	13.6	0.2	20	1	US-08-468-819-29	Sequence 29, Appl
C2367	13.6	0.2	20	1	US-08-124-290-3	Sequence 3, Appl	C2440	13.6	0.2	20	1	US-08-468-819-37	Sequence 37, Appl
C2368	13.6	0.2	20	1	US-08-349-696-17	Sequence 17, Appl	C2441	13.6	0.2	20	1	US-08-468-819-45	Sequence 45, Appl
C2369	13.6	0.2	20	1	US-08-587-209-8	Sequence 8, Appl	C2442	13.6	0.2	20	1	US-08-468-819-65	Sequence 65, Appl

2443	13.6	0.2	20	1	US-08-471-973A-17	Sequence 17, Appl	2516	13.6	0.2	20	1	US-09-288-461-47	Sequence 47, Appl
2444	13.6	0.2	20	1	US-08-889-296A-20	Sequence 20, Appl	2517	13.6	0.2	20	1	US-09-444-053-34	Sequence 34, Appl
2445	13.6	0.2	20	1	US-08-692-787-43	Sequence 43, Appl	2518	13.6	0.2	20	1	US-09-080-704A-17	Sequence 17, Appl
2446	13.6	0.2	20	1	US-08-668-448-5	Sequence 5, Appl1	2519	13.6	0.2	20	1	US-09-435-226-56	Sequence 56, Appl
2447	13.6	0.2	20	1	US-08-540-804-22	Sequence 22, Appl	2520	13.6	0.2	20	1	US-09-490-692-67	Sequence 67, Appl
2448	13.6	0.2	20	1	US-08-218-265-22	Sequence 22, Appl	2521	13.6	0.2	20	1	US-09-490-692-68	Sequence 68, Appl
2449	13.6	0.2	20	1	US-08-529-878B-31	Sequence 31, Appl	2522	13.6	0.2	20	1	US-09-490-692-72	Sequence 72, Appl
2450	13.6	0.2	20	1	US-08-931-072A-39	Sequence 39, Appl	2523	13.6	0.2	20	1	US-09-490-692-125	Sequence 125, App
2451	13.6	0.2	20	1	US-08-458-356-5	Sequence 5, Appl1	2524	13.6	0.2	20	1	US-09-280-805-147	Sequence 147, App
2452	13.6	0.2	20	1	US-08-875-377-2	Sequence 2, Appl1	2525	13.6	0.2	20	1	US-09-075-501-5	Sequence 5, Appl1
2453	13.6	0.2	20	1	US-08-975-211-29	Sequence 29, Appl	2526	13.6	0.2	20	1	US-09-517-584A-73	Sequence 73, Appl
2454	13.6	0.2	20	1	US-08-756-806A-44	Sequence 44, Appl	2527	13.6	0.2	20	1	US-09-046-894-55	Sequence 55, Appl
2455	13.6	0.2	20	1	US-08-756-806A-59	Sequence 59, Appl	2528	13.6	0.2	20	1	US-09-408-257-26	Sequence 26, Appl
2456	13.6	0.2	20	1	US-09-044-506A-14	Sequence 14, Appl	2529	13.6	0.2	20	1	US-09-092-077-31	Sequence 31, Appl
2457	13.6	0.2	20	1	US-08-465-880-22	Sequence 22, Appl	2530	13.6	0.2	20	1	US-09-092-077-33	Sequence 33, Appl
2458	13.6	0.2	20	1	US-08-848-840A-20	Sequence 20, Appl	2531	13.6	0.2	20	1	US-09-101-886B-44	Sequence 44, Appl
2459	13.6	0.2	20	1	US-08-910-408-172	Sequence 172, App	2532	13.6	0.2	20	1	US-09-101-886B-89	Sequence 89, Appl1
2460	13.6	0.2	20	1	US-08-703-136-13	Sequence 13, Appl	2533	13.6	0.2	20	1	US-09-413-304-9	Sequence 9, Appl1
2461	13.6	0.2	20	1	US-08-910-408-189	Sequence 189, App	2534	13.6	0.2	20	1	US-09-244-794A-31	Sequence 31, Appl
2462	13.6	0.2	20	1	US-08-863-639A-72	Sequence 72, Appl	2535	13.6	0.2	20	1	US-08-590-393-22	Sequence 204, App
2463	13.6	0.2	20	1	US-08-863-639A-93	Sequence 93, Appl	2536	13.6	0.2	20	1	US-09-262-773-204	Sequence 17, Appl
2464	13.6	0.2	20	1	US-08-837-201C-63	Sequence 63, Appl	2537	13.6	0.2	20	1	US-09-313-932-17	Sequence 22, Appl
2465	13.6	0.2	20	1	US-08-837-201C-75	Sequence 75, Appl	2538	13.6	0.2	20	1	US-09-313-932-22	Sequence 398, App
2466	13.6	0.2	20	1	US-08-471-025-5	Sequence 5, Appl1	2539	13.6	0.2	20	1	US-09-313-932-358	Sequence 15, Appl
2467	13.6	0.2	20	1	US-08-781-620B-8	Sequence 8, Appl1	2540	13.6	0.2	20	1	US-08-996-069A-15	Sequence 17, Appl
2468	13.6	0.2	20	1	US-08-658-665-5	Sequence 5, Appl1	2541	13.6	0.2	20	1	US-09-038-637-106	Sequence 106, App
2469	13.6	0.2	20	1	US-09-190-982-26	Sequence 26, Appl	2542	13.6	0.2	20	1	US-09-290-577-5	Sequence 5, Appl1
2470	13.6	0.2	20	1	US-09-226-568-11	Sequence 11, Appl	2543	13.6	0.2	20	1	US-09-290-577-22	Sequence 22, Appl
2471	13.6	0.2	20	1	US-08-917-653-1	Sequence 1, Appl1	2544	13.6	0.2	20	1	US-09-371-774-50	Sequence 50, Appl
2472	13.6	0.2	20	1	US-09-035-357-17	Sequence 17, Appl	2545	13.6	0.2	20	1	US-09-560-594-351	Sequence 54, Appl
2473	13.6	0.2	20	1	US-08-809-999D-4	Sequence 4, Appl	2546	13.6	0.2	20	1	US-09-021-701-351	Sequence 351, App
2474	13.6	0.2	20	1	US-08-521-872-22	Sequence 22, Appl	2547	13.6	0.2	20	1	US-09-021-701-353	Sequence 353, App
2475	13.6	0.2	20	1	US-08-473-446-28	Sequence 28, Appl	2548	13.6	0.2	20	1	US-09-021-701-359	Sequence 399, App
2476	13.6	0.2	20	1	US-09-069-637-4	Sequence 4, Appl1	2549	13.6	0.2	20	1	US-09-021-701-400	Sequence 400, App
2477	13.6	0.2	20	1	US-09-366-257-35	Sequence 35, Appl	2550	13.6	0.2	20	1	US-09-021-701-404	Sequence 404, App
2478	13.6	0.2	20	1	US-08-979-269-11	Sequence 11, Appl	2551	13.6	0.2	20	1	US-09-021-701-512	Sequence 512, App
2479	13.6	0.2	20	1	US-08-742-877-11	Sequence 11, Appl	2552	13.6	0.2	20	1	US-09-021-701-550	Sequence 550, App
2480	13.6	0.2	20	1	US-09-106-217-7	Sequence 7, Appl1	2553	13.6	0.2	20	1	US-09-021-701-663	Sequence 663, App
2481	13.6	0.2	20	1	US-09-132-652-23	Sequence 23, Appl	2554	13.6	0.2	20	1	US-09-021-701-664	Sequence 664, App
2482	13.6	0.2	20	1	US-09-111-752-2	Sequence 2, Appl1	2555	13.6	0.2	20	1	US-09-021-701-673	Sequence 673, App
2483	13.6	0.2	20	1	US-08-696-372A-3	Sequence 3, Appl1	2556	13.6	0.2	20	1	US-09-043-303-8	Sequence 8, Appl1
2484	13.6	0.2	20	1	US-08-945-056-14	Sequence 14, Appl	2557	13.6	0.2	20	1	US-08-875-847B-29	Sequence 29, Appl
2485	13.6	0.2	20	1	US-09-166-186-17	Sequence 17, Appl	2558	13.6	0.2	20	1	US-09-007-005-31	Sequence 31, Appl
2486	13.6	0.2	20	1	US-09-166-186-22	Sequence 22, Appl	2559	13.6	0.2	20	1	US-09-487-445-47	Sequence 47, Appl
2487	13.6	0.2	20	1	US-08-961-469A-28	Sequence 28, Appl	2560	13.6	0.2	20	1	US-09-657-481A-37	Sequence 37, Appl
2488	13.6	0.2	20	1	US-09-009-913-259	Sequence 19, Appl	2561	13.6	0.2	20	1	US-09-377-309-76	Sequence 76, Appl
2489	13.6	0.2	20	1	US-09-164-907-19	Sequence 44, Appl	2562	13.6	0.2	20	1	US-08-090-369-12	Sequence 12, Appl
2490	13.6	0.2	20	1	US-09-143-214-44	Sequence 59, Appl	2563	13.6	0.2	20	1	US-09-247-139-31	Sequence 31, Appl
2491	13.6	0.2	20	1	US-08-621-841-45	Sequence 45, Appl	2564	13.6	0.2	20	1	US-08-943-731-513	Sequence 513, App
2492	13.6	0.2	20	1	US-09-344-914-68	Sequence 68, Appl	2565	13.6	0.2	20	1	US-08-460-735-5	Sequence 5, Appl1
2493	13.6	0.2	20	1	US-09-344-914-74	Sequence 74, Appl	2566	13.6	0.2	20	1	US-09-489-866A-49	Sequence 49, Appl
2494	13.6	0.2	20	1	US-09-344-914-75	Sequence 75, Appl	2567	13.6	0.2	20	1	US-09-489-866A-60	Sequence 60, Appl
2495	13.6	0.2	20	1	US-09-344-914-76	Sequence 76, Appl	2568	13.6	0.2	20	1	US-09-085-277-5	Sequence 5, Appl1
2496	13.6	0.2	20	1	US-08-850-347-8	Sequence 8, Appl1	2569	13.6	0.2	20	1	US-09-428-583-70	Sequence 70, Appl
2497	13.6	0.2	20	1	US-09-062-416-27	Sequence 27, Appl	2570	13.6	0.2	20	1	US-09-593-711A-155	Sequence 155, App
2498	13.6	0.2	20	1	US-09-128-494-20	Sequence 20, Appl	2571	13.6	0.2	20	1	US-09-593-711A-160	Sequence 160, App
2499	13.6	0.2	20	1	US-08-990-065-8	Sequence 8, Appl1	2572	13.6	0.2	20	1	US-08-836-031-2	Sequence 2, Appl1
2500	13.6	0.2	20	1	US-08-930-601-5	Sequence 5, Appl1	2573	13.6	0.2	20	1	US-09-430-033-2	Sequence 31, Appl1
2501	13.6	0.2	20	1	US-09-074-357-9	Sequence 9, Appl	2574	13.6	0.2	20	1	US-09-244-793-31	Sequence 4, Appl1
2502	13.6	0.2	20	1	US-09-280-799-52	Sequence 52, Appl	2575	13.6	0.2	20	1	US-09-322-360-4	Sequence 93, Appl
2503	13.6	0.2	20	1	US-09-280-799-175	Sequence 15, App	2576	13.6	0.2	20	1	US-09-484-617-93	Sequence 137, App
2504	13.6	0.2	20	1	US-09-150-805-15	Sequence 17, Appl	2577	13.6	0.2	20	1	US-09-484-617-117	Sequence 151, App
2505	13.6	0.2	20	1	US-09-150-805-17	Sequence 26, Appl	2578	13.6	0.2	20	1	US-08-890-865A-5	Sequence 5, Appl1
2506	13.6	0.2	20	1	US-09-429-323-26	Sequence 30, Appl	2579	13.6	0.2	20	1	US-09-354-133-5	Sequence 5, Appl1
2507	13.6	0.2	20	1	US-09-429-323-30	Sequence 46, Appl	2580	13.6	0.2	20	1	US-09-290-455-5	Sequence 22, Appl
2508	13.6	0.2	20	1	US-08-765-340-19	Sequence 19, Appl	2581	13.6	0.2	20	1	US-09-364-416-63	Sequence 63, Appl
2509	13.6	0.2	20	1	US-08-765-340-64	Sequence 64, Appl	2582	13.6	0.2	20	1	US-09-364-416-75	Sequence 75, Appl
2510	13.6	0.2	20	1	US-08-765-340-64	Sequence 64, Appl	2583	13.6	0.2	20	1	US-09-101-126-10	Sequence 10, Appl
2511	13.6	0.2	20	1	US-08-765-340-64	Sequence 64, Appl	2584	13.6	0.2	20	1	US-09-488-856A-15	Sequence 15, Appl
2512	13.6	0.2	20	1	US-08-765-340-64	Sequence 64, Appl	2585	13.6	0.2	20	1		
2513	13.6	0.2	20	1	US-09-249-215-172	Sequence 172, App	2586	13.6	0.2	20	1		
2514	13.6	0.2	20	1	US-09-249-215-189	Sequence 189, App	2587	13.6	0.2	20	1		
2515	13.6	0.2	20	1	US-09-288-461-23	Sequence 23, Appl	2588	13.6	0.2	20	1		

2589	13.6	0.2	20	1	US-09-290-338-5	Sequence 5, Appl1	2662	13.6	0.2	20	1	US-09-238-710-11	Sequence 31, Appl1
2590	13.6	0.2	20	1	US-09-290-338-22	Sequence 22, Appl1	2663	13.6	0.2	20	1	US-09-358-383C-21	Sequence 21, Appl1
2591	13.6	0.2	20	1	US-09-082-649B-77	Sequence 77, Appl1	2664	13.6	0.2	20	1	US-09-250-000-5	Sequence 5, Appl1
2592	13.6	0.2	20	1	US-09-082-649B-77	Sequence 77, Appl1	2665	13.6	0.2	20	1	US-09-250-000-5	Sequence 5, Appl1
2593	13.6	0.2	20	1	US-09-488-074-3	Sequence 3, Appl1	2666	13.6	0.2	20	1	US-09-389-283-17	Sequence 17, Appl1
2594	13.6	0.2	20	1	US-09-131-831B-4	Sequence 4, Appl1	2667	13.6	0.2	20	1	US-09-972-800A-45	Sequence 45, Appl1
2595	13.6	0.2	20	1	US-09-378-842-29	Sequence 29, Appl1	2668	13.6	0.2	20	1	US-09-535-170-5	Sequence 5, Appl1
2596	13.6	0.2	20	1	US-09-482-971-12	Sequence 12, Appl1	2669	13.6	0.2	20	1	US-09-422-978-4925	Sequence 425, Ap
2597	13.6	0.2	20	1	US-09-248-386-20	Sequence 20, Appl1	2670	13.6	0.2	20	1	US-09-422-978-1168	Sequence 5168, Ap
2598	13.6	0.2	20	1	US-09-561-497-20	Sequence 20, Appl1	2671	13.6	0.2	20	1	US-09-422-978-5234	Sequence 5234, Ap
2599	13.6	0.2	20	1	US-09-561-497-42	Sequence 42, Appl1	2672	13.6	0.2	20	1	US-09-422-978-6127	Sequence 6127, Ap
2600	13.6	0.2	20	1	US-09-733-199A-29	Sequence 29, Appl1	2673	13.6	0.2	20	1	US-09-422-978-6243	Sequence 6243, Ap
2601	13.6	0.2	20	1	US-09-177-437-6	Sequence 6, Appl1	2674	13.6	0.2	20	1	US-09-422-978-8329	Sequence 8329, Ap
2602	13.6	0.2	20	1	US-09-702-246-73	Sequence 73, Appl1	2675	13.6	0.2	20	1	US-09-422-978-8529	Sequence 8529, Ap
2603	13.6	0.2	20	1	US-09-588-950A-6	Sequence 6, Appl1	2676	13.6	0.2	20	1	US-09-422-978-9857	Sequence 9857, Ap
2604	13.6	0.2	20	1	US-09-135-202-17	Sequence 17, Appl1	2677	13.6	0.2	20	1	US-09-422-978-10500	Sequence 10500, A
2605	13.6	0.2	20	1	US-09-844-634-54	Sequence 54, Appl1	2678	13.6	0.2	20	1	US-09-422-978-10511	Sequence 10511, A
2606	13.6	0.2	20	1	US-09-844-634-56	Sequence 56, Appl1	2679	13.6	0.2	20	1	US-09-422-978-11697	Sequence 11697, A
2607	13.6	0.2	20	1	US-09-844-634-159	Sequence 159, App	2680	13.6	0.2	20	1	US-08-894-454-72	Sequence 72, Appl1
2608	13.6	0.2	20	1	US-09-506-073-46	Sequence 46, Appl1	2681	13.6	0.2	20	1	US-09-060-299-240	Sequence 240, App
2609	13.6	0.2	20	1	US-09-506-073-61	Sequence 61, Appl1	2682	13.6	0.2	20	1	US-09-705-267A-57	Sequence 57, Appl1
2610	13.6	0.2	20	1	US-09-506-073-71	Sequence 71, Appl1	2683	13.6	0.2	20	1	US-09-705-267A-113	Sequence 113, App
2611	13.6	0.2	20	1	US-09-817-856-9	Sequence 9, Appl1	2684	13.6	0.2	20	1	US-09-402-923A-240	Sequence 240, App
2612	13.6	0.2	20	1	US-09-370-398-13	Sequence 53, Appl1	2685	13.6	0.2	20	1	US-09-198-452A-1563	Sequence 1563, Ap
2613	13.6	0.2	20	1	US-09-657-452A-53	Sequence 53, Appl1	2686	13.6	0.2	20	1	US-09-198-452A-1681	Sequence 1681, Ap
2614	13.6	0.2	20	1	US-09-487-792-42	Sequence 42, Appl1	2687	13.6	0.2	20	1	US-09-198-452A-1880	Sequence 1880, Ap
2615	13.6	0.2	20	1	US-09-661-753-37	Sequence 37, Appl1	2688	13.6	0.2	20	1	US-09-198-452A-2085	Sequence 2085, Ap
2616	13.6	0.2	20	1	US-09-780-175-37	Sequence 37, Appl1	2689	13.6	0.2	20	1	US-09-198-452A-2147	Sequence 2147, Ap
2617	13.6	0.2	20	1	US-09-780-175-66	Sequence 66, Appl1	2690	13.6	0.2	20	1	US-09-198-452A-2339	Sequence 2339, Ap
2618	13.6	0.2	20	1	US-09-907-843-35	Sequence 35, Appl1	2691	13.6	0.2	20	1	US-09-198-452A-2492	Sequence 2492, Ap
2619	13.6	0.2	20	1	US-09-907-843-70	Sequence 70, Appl1	2692	13.6	0.2	20	1	US-09-198-452A-2593	Sequence 2593, Ap
2620	13.6	0.2	20	1	US-09-470-443-90	Sequence 90, Appl1	2693	13.6	0.2	20	1	US-09-198-452A-3426	Sequence 3426, Ap
2621	13.6	0.2	20	1	US-09-791-211-75	Sequence 75, Appl1	2694	13.6	0.2	20	1	US-09-198-452A-3526	Sequence 3526, Ap
2622	13.6	0.2	20	1	US-09-851-062-82	Sequence 82, Appl1	2695	13.6	0.2	20	1	US-09-198-452A-4058	Sequence 4058, Ap
2623	13.6	0.2	20	1	US-09-517-467B-57	Sequence 57, Appl1	2696	13.6	0.2	20	1	US-09-198-452A-4655	Sequence 4627, Ap
2624	13.6	0.2	20	1	US-09-517-467B-125	Sequence 125, App	2697	13.6	0.2	20	1	US-09-198-452A-4703	Sequence 4703, Ap
2625	13.6	0.2	20	1	US-09-517-467B-274	Sequence 274, App	2698	13.6	0.2	20	1	US-09-198-452A-4705	Sequence 4705, Ap
2626	13.6	0.2	20	1	US-08-275-951-27	Sequence 27, Appl1	2699	13.6	0.2	20	1	US-09-198-452A-4715	Sequence 4715, Ap
2627	13.6	0.2	20	1	US-08-275-951-28	Sequence 28, Appl1	2700	13.6	0.2	20	1	US-09-198-452A-4717	Sequence 4717, Ap
2628	13.6	0.2	20	1	US-08-275-951-29	Sequence 29, Appl1	2701	13.6	0.2	20	1	US-09-198-452A-4715	Sequence 4715, Ap
2629	13.6	0.2	20	1	US-08-275-951-30	Sequence 30, Appl1	2702	13.6	0.2	20	1	US-09-198-452A-4715	Sequence 4715, Ap
2630	13.6	0.2	20	1	US-08-275-951-31	Sequence 31, Appl1	2703	13.6	0.2	20	1	US-09-198-452A-4808	Sequence 4808, Ap
2631	13.6	0.2	20	1	US-08-802-331-32	Sequence 32, Appl1	2704	13.6	0.2	20	1	US-09-198-452A-5028	Sequence 5028, Ap
2632	13.6	0.2	20	1	US-09-920-672-33	Sequence 33, Appl1	2705	13.6	0.2	20	1	US-09-198-452A-5087	Sequence 5087, Ap
2633	13.6	0.2	20	1	US-09-920-672-51	Sequence 51, Appl1	2706	13.6	0.2	20	1	US-09-198-452A-5266	Sequence 5266, Ap
2634	13.6	0.2	20	1	US-08-626-285-26	Sequence 26, Appl1	2707	13.6	0.2	20	1	US-09-198-452A-5520	Sequence 5520, Ap
2635	13.6	0.2	20	1	US-09-679-185-6	Sequence 6, Appl1	2708	13.6	0.2	20	1	US-09-198-452A-5527	Sequence 5527, Ap
2636	13.6	0.2	20	1	US-09-531-000-64	Sequence 64, Appl1	2709	13.6	0.2	20	1	US-09-198-452A-5565	Sequence 5565, Ap
2637	13.6	0.2	20	1	US-09-531-000-64	Sequence 64, Appl1	2710	13.6	0.2	20	1	US-09-198-452A-5565	Sequence 5565, Ap
2638	13.6	0.2	20	1	US-09-780-049-86	Sequence 86, Appl1	2711	13.6	0.2	20	1	US-09-198-452A-5857	Sequence 5857, Ap
2639	13.6	0.2	20	1	US-09-291-129-2	Sequence 2, Appl1	2712	13.6	0.2	20	1	US-09-198-452A-6061	Sequence 6061, Ap
2640	13.6	0.2	20	1	US-09-291-129-13	Sequence 13, Appl1	2713	13.6	0.2	20	1	US-09-198-452A-6061	Sequence 6061, Ap
2641	13.6	0.2	20	1	US-09-475-947A-56	Sequence 56, Appl1	2714	13.6	0.2	20	1	US-09-198-452A-6585	Sequence 6585, Ap
2642	13.6	0.2	20	1	US-09-908-594-42	Sequence 42, Appl1	2715	13.6	0.2	20	1	US-09-198-452A-6585	Sequence 6585, Ap
2643	13.6	0.2	20	1	US-09-706-197-84	Sequence 84, Appl1	2716	13.6	0.2	20	1	US-09-198-452A-6585	Sequence 6585, Ap
2644	13.6	0.2	20	1	US-09-698-505A-36	Sequence 36, Appl1	2717	13.6	0.2	20	1	US-09-309-595-62	Sequence 59, Appl1
2645	13.6	0.2	20	1	US-09-920-668-52	Sequence 32, Appl1	2718	13.6	0.2	20	1	US-09-594-594A-5	Sequence 5, Appl1
2646	13.6	0.2	20	1	US-10-090-190-13	Sequence 13, Appl1	2719	13.6	0.2	20	1	US-09-594-594A-22	Sequence 22, Appl1
2647	13.6	0.2	20	1	US-09-213-383-29	Sequence 29, Appl1	2720	13.6	0.2	20	1	US-09-081-185-63	Sequence 63, Appl1
2648	13.6	0.2	20	1	US-09-213-383-37	Sequence 37, Appl1	2721	13.6	0.2	20	1	US-09-136-159A-5	Sequence 5, Appl1
2649	13.6	0.2	20	1	US-09-213-383-45	Sequence 45, Appl1	2722	13.6	0.2	20	1	US-09-823-634A-8	Sequence 8, Appl1
2650	13.6	0.2	20	1	US-09-213-383-65	Sequence 65, Appl1	2723	13.6	0.2	20	1	US-09-823-634A-9	Sequence 9, Appl1
2651	13.6	0.2	20	1	US-09-844-521-67	Sequence 67, Appl1	2724	13.6	0.2	20	1	US-09-823-634A-10	Sequence 10, Appl1
2652	13.6	0.2	20	1	US-09-629-644A-131	Sequence 131, App	2725	13.6	0.2	20	1	US-09-823-634A-11	Sequence 11, Appl1
2653	13.6	0.2	20	1	US-09-629-644A-131	Sequence 131, App	2726	13.6	0.2	20	1	US-09-823-634A-12	Sequence 12, Appl1
2654	13.6	0.2	20	1	US-08-545-573A-31	Sequence 31, Appl1	2727	13.6	0.2	20	1	US-09-823-634A-13	Sequence 13, Appl1
2655	13.6	0.2	20	1	US-08-559-284-26	Sequence 26, Appl1	2728	13.6	0.2	20	1	US-09-823-634A-14	Sequence 14, Appl1
2656	13.6	0.2	20	1	US-09-898-361-87	Sequence 87, Appl1	2729	13.6	0.2	20	1	US-09-823-634A-15	Sequence 15, Appl1
2657	13.6	0.2	20	1	US-09-898-361-151	Sequence 151, App	2730	13.6	0.2	20	1	US-09-823-634A-16	Sequence 16, Appl1
2658	13.6	0.2	20	1	US-09-657-346A-59	Sequence 59, Appl1	2731	13.6	0.2	20	1	US-09-823-634A-17	Sequence 17, Appl1
2659	13.6	0.2	20	1	US-09-657-346A-70	Sequence 70, Appl1	2732	13.6	0.2	20	1	US-09-823-647B-8	Sequence 8, Appl1
2660	13.6	0.2	20	1	US-09-668-313A-43	Sequence 43, Appl1	2733	13.6	0.2	20	1	US-09-823-647B-9	Sequence 9, Appl1
2661	13.6	0.2	20	1	US-09-668-313A-75	Sequence 75, Appl1	2734	13.6	0.2	20	1	US-09-823-647B-10	Sequence 10, Appl1

2735	13.6	0.2	20	1	US-09-823-647B-11	Sequence 11, Appl	2808	13.4	0.2	15	1	US-08-832-021-38	Sequence 38, Appl
c2736	13.6	0.2	20	1	US-09-823-647B-12	Sequence 12, Appl	2809	13.4	0.2	15	1	US-08-832-021-44	Sequence 44, Appl
c2737	13.6	0.2	20	1	US-09-823-647B-13	Sequence 13, Appl	2810	13.4	0.2	15	1	US-08-832-021-48	Sequence 48, Appl
c2738	13.6	0.2	20	1	US-09-823-647B-14	Sequence 14, Appl	2811	13.4	0.2	15	1	US-08-832-021-50	Sequence 50, Appl
c2739	13.6	0.2	20	1	US-09-823-647B-15	Sequence 15, Appl	2812	13.4	0.2	15	1	US-08-832-021-52	Sequence 52, Appl
c2740	13.6	0.2	20	1	US-09-823-647B-16	Sequence 16, Appl	2813	13.4	0.2	15	1	US-08-832-021-54	Sequence 54, Appl
c2741	13.6	0.2	20	1	US-09-823-647B-17	Sequence 17, Appl	2814	13.4	0.2	15	1	US-08-832-021-55	Sequence 55, Appl
2742	13.6	0.2	20	1	US-09-825-497A-22	Sequence 29, Appl	2815	13.4	0.2	15	1	US-08-832-021-56	Sequence 56, Appl
2743	13.6	0.2	20	1	US-10-072-094-79	Sequence 72, Appl	2816	13.4	0.2	15	1	US-08-832-021-58	Sequence 58, Appl
2744	13.6	0.2	20	1	US-09-780-045-24	Sequence 24, Appl	2817	13.4	0.2	15	1	US-08-832-021-59	Sequence 59, Appl
2745	13.6	0.2	20	1	US-09-689-065B-10	Sequence 10, Appl	2818	13.4	0.2	15	1	US-08-832-021-60	Sequence 60, Appl
2746	13.6	0.2	20	1	US-08-944-410-7	Sequence 7, Appl1	c2819	13.4	0.2	15	1	US-08-913-833-25	Sequence 25, Appl
c2747	13.6	0.2	20	1	US-09-526-193A-79	Sequence 79, Appl	2820	13.4	0.2	15	1	US-09-071-884-359	Sequence 359, App
c2748	13.6	0.2	20	1	US-09-434-840-16	Sequence 16, Appl	2821	13.4	0.2	15	1	US-09-180-437-104	Sequence 104, App
c2749	13.6	0.2	20	1	US-08-754-211B-8	Sequence 8, Appl1	2822	13.4	0.2	15	1	US-09-054-833-28	Sequence 28, Appl
c2750	13.6	0.2	20	1	US-09-916-963-5	Sequence 5, Appl1	c2823	13.4	0.2	15	1	US-09-580-799C-35	Sequence 25, Appl
c2751	13.6	0.2	20	1	US-09-664-846A-2	Sequence 2, Appl1	c2824	13.4	0.2	15	1	US-09-081-646-207	Sequence 207, App
2752	13.6	0.2	20	1	US-09-664-846A-2	Sequence 161, App	c2825	13.4	0.2	15	1	US-09-081-646-788	Sequence 788, App
c2753	13.6	0.2	20	1	US-09-092-218-3	Sequence 3, Appl	c2826	13.4	0.2	15	1	US-08-618-834C-6	Sequence 6, Appl1
2754	13.6	0.2	20	1	US-09-980-052-93	Sequence 93, Appl	c2827	13.4	0.2	15	1	US-09-031-953-7	Sequence 7, Appl1
2755	13.6	0.2	20	1	US-09-495-714C-7	Sequence 7, Appl1	2828	13.4	0.2	15	1	US-09-475-947A-164	Sequence 164, App
c2756	13.6	0.2	20	1	PCT-US91-05742-9	Sequence 9, Appl1	2829	13.4	0.2	15	1	US-09-640-933-28	Sequence 28, Appl
c2757	13.6	0.2	20	1	PCT-US91-05742-11	Sequence 11, Appl	2830	13.4	0.2	15	1	US-09-491-356C-19	Sequence 19, Appl
c2758	13.6	0.2	20	1	PCT-US93-04863-23	Sequence 23, Appl	2831	13.4	0.2	15	1	PCT-US91-01574-30	Sequence 20, Appl
c2759	13.6	0.2	20	1	PCT-US95-04477-60	Sequence 60, Appl	2832	13.4	0.2	16	1	US-08-753-147-188	Sequence 188, App
c2760	13.6	0.2	20	1	PCT-US95-06379-36	Sequence 36, Appl	c2833	13.4	0.2	16	1	US-08-173-489C-126	Sequence 126, App
2761	13.6	0.2	20	1	PCT-US95-07111A-44	Sequence 44, Appl	2834	13.4	0.2	16	1	US-08-770-238A-62	Sequence 62, Appl
c2762	13.6	0.2	20	1	PCT-US95-07744A-55	Sequence 55, Appl	2835	13.4	0.2	16	1	US-08-454-098-8	Sequence 8, Appl1
c2763	13.6	0.2	20	1	PCT-US95-1418-40	Sequence 40, Appl	2836	13.4	0.2	16	1	US-08-645-411C-1	Sequence 1, Appl1
2765	13.6	0.2	20	1	PCT-US95-15327-40	Sequence 40, Appl	c2837	13.4	0.2	16	1	US-08-645-411C-2	Sequence 2, Appl1
c2766	13.6	0.2	20	1	PCT-US96-00331-10	Sequence 10, Appl	2838	13.4	0.2	16	1	US-08-645-411C-6	Sequence 6, Appl1
c2767	13.6	0.2	21	1	US-08-435-896-13	Sequence 5, Appl1	2839	13.4	0.2	16	1	US-08-645-411C-7	Sequence 7, Appl1
c2768	13.6	0.2	21	1	US-08-933-143-13	Sequence 13, Appl	2840	13.4	0.2	16	1	US-08-645-411C-8	Sequence 8, Appl1
2770	13.6	0.2	21	1	US-09-082-343-13	Sequence 13, Appl	c2841	13.4	0.2	16	1	US-08-545-411C-9	Sequence 9, Appl1
c2771	13.6	0.2	21	1	US-08-863-639A-10	Sequence 10, Appl	2842	13.4	0.2	16	1	US-09-371-772B-5982	Sequence 5982, Ap
c2772	13.6	0.2	21	1	US-08-863-639A-13	Sequence 13, Appl	2843	13.4	0.2	16	1	US-09-479-005A-95	Sequence 95, Appl
c2773	13.6	0.2	21	1	US-08-416-214A-12	Sequence 12, Appl	c2844	13.4	0.2	16	1	US-09-479-005A-987	Sequence 487, App
c2774	13.6	0.2	21	1	US-09-082-253-13	Sequence 13, Appl	2845	13.4	0.2	16	1	PCT-US96-01600-8	Sequence 8, Appl1
c2775	13.6	0.2	21	1	US-09-509-015-13	Sequence 13, Appl	2846	13.4	0.2	17	1	US-08-045-264A-3	Sequence 3, Appl1
c2776	13.6	0.2	21	1	PCT-US96-08235-13	Sequence 13, Appl	c2847	13.4	0.2	17	1	US-08-281-940-24	Sequence 24, Appl
c2777	13.6	0.2	21	1	US-09-475-947A-119	Sequence 119, App	c2848	13.4	0.2	17	1	US-08-373-124A-316	Sequence 316, App
2778	13.6	0.2	24	1	US-09-164-249B-6	Sequence 6, Appl1	2849	13.4	0.2	17	1	US-08-373-124A-530	Sequence 530, App
c2779	13.6	0.2	24	1	US-09-721-154-2	Sequence 2, Appl1	c2850	13.4	0.2	17	1	US-08-373-124A-974	Sequence 974, App
c2780	13.6	0.2	24	1	US-08-014-943A-11	Sequence 11, Appl	c2851	13.4	0.2	17	1	US-08-373-124A-1421	Sequence 1421, Ap
c2781	13.6	0.2	24	1	US-08-486-421-46	Sequence 46, Appl	2852	13.4	0.2	17	1	US-08-373-124A-1969	Sequence 1969, Ap
c2782	13.6	0.2	24	1	US-08-470-911-46	Sequence 46, Appl	c2853	13.4	0.2	17	1	US-08-373-124A-2051	Sequence 2051, Ap
c2783	13.6	0.2	24	1	US-08-486-809-46	Sequence 85, Appl	2854	13.4	0.2	17	1	US-08-373-124A-2055	Sequence 2055, Ap
2784	13.6	0.2	30	1	US-08-181-371A-85	Sequence 85, Appl	c2855	13.4	0.2	17	1	US-08-373-124A-2055	Sequence 2055, Ap
2785	13.6	0.2	30	1	US-08-449-315-85	Sequence 85, Appl	c2856	13.4	0.2	17	1	US-08-373-124A-2055	Sequence 2055, Ap
2786	13.6	0.2	30	1	US-08-444-803-85	Sequence 85, Appl	c2857	13.4	0.2	17	1	US-08-327-526A-28	Sequence 28, Appl
2787	13.6	0.2	30	1	US-08-449-043-85	Sequence 85, Appl	c2858	13.4	0.2	17	1	US-08-327-526A-28	Sequence 28, Appl
2788	13.6	0.2	30	1	US-08-456-265A-85	Sequence 85, Appl	c2859	13.4	0.2	17	1	US-08-327-526A-28	Sequence 28, Appl
2789	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	c2860	13.4	0.2	17	1	US-08-327-526A-28	Sequence 28, Appl
2790	13.6	0.2	30	1	US-08-455-416-85	Sequence 85, Appl	2861	13.4	0.2	17	1	US-08-435-628-530	Sequence 530, App
2791	13.6	0.2	30	1	US-08-454-876-85	Sequence 85, Appl	c2862	13.4	0.2	17	1	US-08-435-628-974	Sequence 974, App
2792	13.6	0.2	30	1	US-08-457-364-85	Sequence 85, Appl	2863	13.4	0.2	17	1	US-08-435-628-1421	Sequence 1421, Ap
2793	13.6	0.2	30	1	US-08-456-262-85	Sequence 85, Appl	c2864	13.4	0.2	17	1	US-08-435-628-1969	Sequence 1969, Ap
2794	13.6	0.2	30	1	US-08-456-240-85	Sequence 85, Appl	c2865	13.4	0.2	17	1	US-08-435-628-2051	Sequence 2051, Ap
2795	13.6	0.2	30	1	US-08-455-736-85	Sequence 85, Appl	c2866	13.4	0.2	17	1	US-08-435-628-2055	Sequence 2055, Ap
2796	13.6	0.2	30	1	US-08-971-217-85	Sequence 85, Appl	c2867	13.4	0.2	17	1	US-08-435-628-2055	Sequence 2055, Ap
2797	13.6	0.2	30	1	US-09-350-600-85	Sequence 85, Appl	c2868	13.4	0.2	17	1	US-08-435-628-2055	Sequence 2055, Ap
2798	13.6	0.2	30	1	US-09-906-234-85	Sequence 85, Appl	c2869	13.4	0.2	17	1	US-08-435-628-2055	Sequence 2055, Ap
c2799	13.6	0.2	32	1	US-08-522-623-14	Sequence 14, Appl	c2870	13.4	0.2	17	1	US-08-435-628-2055	Sequence 2055, Ap
c2800	13.6	0.2	32	1	PCT-US93-03256-14	Sequence 14, Appl	2871	13.4	0.2	17	1	US-08-173-489C-95	Sequence 95, Appl
c2801	13.4	0.2	15	1	US-08-580-242-3	Sequence 3, Appl1	2872	13.4	0.2	17	1	US-07-923-871C-7	Sequence 7, Appl1
2802	13.4	0.2	15	1	US-08-292-620A-359	Sequence 359, App	c2873	13.4	0.2	17	1	US-08-472-802C-33	Sequence 33, Appl1
2803	13.4	0.2	15	1	US-08-173-489C-61	Sequence 61, App	c2874	13.4	0.2	17	1	US-08-531-137B-28	Sequence 28, Appl
2804	13.4	0.2	15	1	US-07-923-871C-20	Sequence 20, Appl	c2875	13.4	0.2	17	1	US-08-825-487A-95	Sequence 95, Appl
c2805	13.4	0.2	15	1	US-08-874-266-7	Sequence 7, Appl1	2876	13.4	0.2	17	1	US-08-985-162-116	Sequence 116, App
2806	13.4	0.2	15	1	US-08-893-204C-2	Sequence 2, Appl1	2877	13.4	0.2	17	1	US-08-985-162-617	Sequence 617, App
2807	13.4	0.2	15	1	US-08-893-204C-2	Sequence 26, Appl	2878	13.4	0.2	17	1	US-08-988-099-134	Sequence 134, App
							c2879	13.4	0.2	17	1	US-09-071-845-1868	Sequence 1868, Ap
							c2880	13.4	0.2	17	1	US-09-071-845-1912	Sequence 1912, Ap

c2881	13.4	0.2	17	1	US-09-158-765-28	Sequence 28, Appl	2954	13.4	0.2	18	1	US-09-054-830-18	Sequence 18, Appl
2882	13.4	0.2	17	1	US-08-584-040-2167	Sequence 2187, Ap	2955	13.4	0.2	18	1	US-09-487-444-36	Sequence 36, Appl
2883	13.4	0.2	17	1	US-08-584-040-2188	Sequence 2188, Ap	2956	13.4	0.2	18	1	US-09-474-922A-57	Sequence 57, Appl
2884	13.4	0.2	17	1	US-08-584-040-2189	Sequence 2189, Ap	c2957	13.4	0.2	18	1	US-09-034-205-64	Sequence 64, Appl
2885	13.4	0.2	17	1	US-08-584-040-2199	Sequence 2739, Ap	c2958	13.4	0.2	18	1	US-09-050-155-1	Sequence 1, Appl
2886	13.4	0.2	17	1	US-08-584-040-2807	Sequence 2807, Ap	c2959	13.4	0.2	18	1	US-09-269-345-1	Sequence 1, Appl
c2887	13.4	0.2	17	1	US-08-584-040-5862	Sequence 5862, Ap	c2960	13.4	0.2	18	1	US-09-313-933-169	Sequence 169, App
c2888	13.4	0.2	17	1	US-09-474-432B-8686	Sequence 866, App	c2961	13.4	0.2	18	1	US-09-313-933-170	Sequence 170, App
c2889	13.4	0.2	17	1	US-09-057-351-33	Sequence 33, Appl	c2962	13.4	0.2	18	1	US-09-313-933-171	Sequence 171, App
2890	13.4	0.2	17	1	US-09-371-772B-732	Sequence 732, App	c2963	13.4	0.2	18	1	US-09-313-933-172	Sequence 172, App
2891	13.4	0.2	17	1	US-09-371-772B-733	Sequence 733, App	c2964	13.4	0.2	18	1	US-09-677-218B-64	Sequence 64, Appl
2892	13.4	0.2	17	1	US-09-371-772B-734	Sequence 734, App	c2965	13.4	0.2	18	1	US-09-677-197-64	Sequence 64, Appl
2893	13.4	0.2	17	1	US-09-371-772B-1263	Sequence 1263, Ap	2966	13.4	0.2	18	1	US-09-431-385-18	Sequence 18, Appl
2894	13.4	0.2	17	1	US-09-371-772B-1331	Sequence 1331, Ap	2967	13.4	0.2	18	1	US-09-319-588C-51	Sequence 51, Appl
c2895	13.4	0.2	17	1	US-09-371-772B-2568	Sequence 2568, Ap	2968	13.4	0.2	18	1	US-09-319-588C-60	Sequence 80, Appl
2896	13.4	0.2	17	1	US-09-371-772B-4186	Sequence 4186, Ap	2969	13.4	0.2	18	1	US-09-216-393B-114	Sequence 314, App
2897	13.4	0.2	17	1	US-09-371-772B-5287	Sequence 5287, Ap	2970	13.4	0.2	18	1	US-09-197-224-13	Sequence 13, App
2898	13.4	0.2	17	1	US-09-371-772B-5594	Sequence 5594, Ap	2971	13.4	0.2	18	1	US-09-422-978-608	Sequence 608, App
c2899	13.4	0.2	17	1	US-09-476-071-28	Sequence 28, Appl	c2972	13.4	0.2	18	1	US-09-422-978-7515	Sequence 7515, Ap
c2900	13.4	0.2	17	1	US-09-476-387-895	Sequence 895, App	c2973	13.4	0.2	18	1	US-09-422-978-7519	Sequence 7519, Ap
2901	13.4	0.2	17	1	US-09-401-063-116	Sequence 116, App	2974	13.4	0.2	18	1	US-09-422-978-8959	Sequence 9179, Ap
2902	13.4	0.2	17	1	US-09-401-063-617	Sequence 617, App	c2975	13.4	0.2	18	1	US-09-422-978-9179	Sequence 9179, Ap
2903	13.4	0.2	17	1	US-09-827-998-102	Sequence 102, App	c2976	13.4	0.2	18	1	US-09-422-978-11146	Sequence 11146, A
2904	13.4	0.2	17	1	US-09-827-998-103	Sequence 103, App	2977	13.4	0.2	18	1	US-09-230-655-67	Sequence 67, Appl
2905	13.4	0.2	17	1	US-09-827-998-104	Sequence 104, App	2978	13.4	0.2	18	1	US-09-197-221-13	Sequence 13, Appl
2906	13.4	0.2	17	1	US-09-827-998-371	Sequence 371, App	2979	13.4	0.2	18	1	US-09-572-392A-13	Sequence 13, Appl
2907	13.4	0.2	17	1	US-09-827-998-372	Sequence 372, App	2980	13.4	0.2	18	1	US-09-723-756-13	Sequence 13, Appl
2908	13.4	0.2	17	1	US-09-827-998-373	Sequence 373, App	2981	13.4	0.2	18	1	US-09-532-894-13	Sequence 13, Appl
2909	13.4	0.2	17	1	US-09-866-108A-5551	Sequence 551, App	2982	13.4	0.2	18	1	US-09-710-693-13	Sequence 13, Appl
2910	13.4	0.2	17	1	US-09-866-108A-5552	Sequence 552, App	2983	13.4	0.2	18	1	PCT-US91-03056-7	Sequence 7, Appl
c2911	13.4	0.2	17	1	US-09-866-108A-2191	Sequence 2191, Ap	c2984	13.4	0.2	18	1	PCT-US91-03056-10	Sequence 10, Appl
c2912	13.4	0.2	17	1	US-09-866-108A-2194	Sequence 2194, Ap	c2985	13.4	0.2	19	1	US-08-127-954-47	Sequence 47, Appl
c2913	13.4	0.2	17	1	US-09-866-108A-2657	Sequence 2657, Ap	2986	13.4	0.2	19	1	US-08-255-892-66	Sequence 66, Appl
c2914	13.4	0.2	17	1	US-09-866-108A-5549	Sequence 5549, Ap	c2987	13.4	0.2	19	1	US-08-257-077-106	Sequence 106, App
c2915	13.4	0.2	17	1	US-09-866-108A-5550	Sequence 5550, Ap	c2988	13.4	0.2	19	1	US-08-184-009-124	Sequence 124, App
2916	13.4	0.2	17	1	US-09-866-108A-6257	Sequence 6257, Ap	2989	13.4	0.2	19	1	US-08-389-360-7	Sequence 7, Appl
2917	13.4	0.2	17	1	US-09-866-108A-6258	Sequence 6258, Ap	c2990	13.4	0.2	19	1	US-08-458-356-124	Sequence 124, App
2918	13.4	0.2	17	1	US-09-866-108A-6259	Sequence 6259, Ap	2991	13.4	0.2	19	1	US-09-033-328-7	Sequence 7, Appl
c2919	13.4	0.2	17	1	US-09-866-108A-7070	Sequence 7070, Ap	2992	13.4	0.2	19	1	US-09-092-077-15	Sequence 15, Appl
2920	13.4	0.2	17	1	US-09-866-108A-7588	Sequence 7588, Ap	2993	13.4	0.2	19	1	US-09-183-931-16	Sequence 16, Appl
2921	13.4	0.2	17	1	US-09-866-108A-7589	Sequence 7589, Ap	c2994	13.4	0.2	19	1	US-08-460-793-114	Sequence 124, App
c2922	13.4	0.2	17	1	US-09-866-108A-7583	Sequence 7583, Ap	c2995	13.4	0.2	19	1	US-09-338-907-464	Sequence 464, App
c2923	13.4	0.2	17	1	US-09-866-108A-8872	Sequence 8872, Ap	c2996	13.4	0.2	19	1	US-09-218-207-464	Sequence 464, App
c2924	13.4	0.2	17	1	US-09-866-108A-8873	Sequence 8873, Ap	2997	13.4	0.2	19	1	US-09-705-160-16	Sequence 16, Appl
c2925	13.4	0.2	17	1	US-09-866-108A-8874	Sequence 8874, Ap	c2998	13.4	0.2	19	1	US-09-345-882-106	Sequence 106, App
2926	13.4	0.2	17	1	US-09-866-108A-9377	Sequence 9377, Ap	2999	13.4	0.2	19	1	US-09-662-402A-34	Sequence 34, Appl
2927	13.4	0.2	17	1	US-09-866-108A-9378	Sequence 9378, Ap	3000	13.4	0.2	19	1	US-09-435-524-7	Sequence 7, Appl
2928	13.4	0.2	17	1	US-09-866-108A-9379	Sequence 9379, Ap	c3001	13.4	0.2	19	1	US-09-422-978-4186	Sequence 124, App
2929	13.4	0.2	17	1	PCT-US91-01574-7	Sequence 7, Appl	3002	13.4	0.2	19	1	US-09-533-370-124	Sequence 4186, App
c2931	13.4	0.2	18	1	PCT-US91-03680-7	Sequence 7, Appl	c3003	13.4	0.2	19	1	US-09-422-978-4425	Sequence 4425, Ap
2932	13.4	0.2	18	1	US-07-766-751-2	Sequence 2, Appl	3004	13.4	0.2	19	1	US-09-422-978-4425	Sequence 4425, Ap
c2933	13.4	0.2	18	1	US-08-170-095B-31	Sequence 31, Appl	3005	13.4	0.2	19	1	US-09-422-978-4423	Sequence 4923, Ap
c2934	13.4	0.2	18	1	US-08-170-095B-34	Sequence 34, Appl	3006	13.4	0.2	19	1	US-09-422-978-5928	Sequence 5928, Ap
2934	13.4	0.2	18	1	US-08-216-276A-7	Sequence 7, Appl	3007	13.4	0.2	19	1	US-09-422-978-6597	Sequence 6597, Ap
c2935	13.4	0.2	18	1	US-08-216-276A-10	Sequence 10, Appl	3008	13.4	0.2	19	1	US-09-422-978-8611	Sequence 8611, Ap
c2936	13.4	0.2	18	1	US-08-390-850-1122	Sequence 1122, Ap	3009	13.4	0.2	19	1	US-09-422-978-8930	Sequence 8930, Ap
2937	13.4	0.2	18	1	US-08-396-866-31	Sequence 31, Appl	c3010	13.4	0.2	19	1	US-09-422-978-9853	Sequence 9853, Ap
c2938	13.4	0.2	18	1	US-08-396-866-34	Sequence 34, Appl	3011	13.4	0.2	19	1	US-09-422-978-9853	Sequence 10308, A
2939	13.4	0.2	18	1	US-08-363-240A-1112	Sequence 1112, Ap	3012	13.4	0.2	19	1	US-09-382-497-7	Sequence 7, Appl
c2940	13.4	0.2	18	1	US-08-363-240A-1223	Sequence 1223, Ap	3013	13.4	0.2	19	1	US-09-747-391-164	Sequence 164, App
c2941	13.4	0.2	18	1	US-08-435-634-1122	Sequence 1122, Ap	c3014	13.4	0.2	19	1	PCT-US91-03680-2	Sequence 2, Appl
2942	13.4	0.2	18	1	US-08-627-254C-21	Sequence 21, Appl	c3015	13.4	0.2	19	1	PCT-US91-03680-9	Sequence 9, Appl
2943	13.4	0.2	18	1	US-08-244-597-13	Sequence 13, Appl	c3016	13.4	0.2	20	1	US-08-487-141B-19	Sequence 19, Appl
2944	13.4	0.2	18	1	US-09-212-771-28	Sequence 28, Appl	c3017	13.4	0.2	20	1	US-08-927-561-19	Sequence 19, Appl
2945	13.4	0.2	18	1	US-09-203-860-75	Sequence 75, Appl	c3018	13.4	0.2	20	1	PCT-US96-09388-19	Sequence 19, Appl
2946	13.4	0.2	18	1	US-09-200-141-18	Sequence 18, Appl	c3019	13.4	0.2	20	1	US-08-275-951-46	Sequence 46, Appl
c2948	13.4	0.2	18	1	US-08-945-654-16	Sequence 16, Appl	c3020	13.4	0.2	20	1	US-09-358-383C-21	Sequence 21, Appl
c2949	13.4	0.2	18	1	US-09-166-186-169	Sequence 169, App	3021	13.4	0.2	20	1	US-07-984-044A-9	Sequence 9, Appl
c2950	13.4	0.2	18	1	US-09-166-186-170	Sequence 170, App	3022	13.4	0.2	20	1	US-08-071-601-15	Sequence 15, Appl
c2951	13.4	0.2	18	1	US-09-166-186-171	Sequence 171, App	c3023	13.4	0.2	20	1	US-08-271-942A-106	Sequence 106, App
2952	13.4	0.2	18	1	US-09-166-186-172	Sequence 172, App	c3024	13.4	0.2	20	1	US-07-977-284A-116	Sequence 116, App
c2953	13.4	0.2	18	1	US-09-166-186-172	Sequence 172, App	3025	13.4	0.2	20	1	US-07-977-284A-118	Sequence 118, App
2954	13.4	0.2	18	1	US-09-289-466-84	Sequence 84, Appl	3026	13.4	0.2	20	1	US-08-250-856A-15	Sequence 15, Appl

c3027	13.4	0.2	20	1	US-08-118-441-3	Sequence 3, Appl1	c3100	13.4	0.2	20	1	US-09-021-701-665	Sequence 665, App
3028	13.4	0.2	20	1	US-08-222-177A-237	Sequence 237, App	c3101	13.4	0.2	20	1	US-09-021-701-666	Sequence 666, App
3029	13.4	0.2	20	1	US-08-222-177A-285	Sequence 285, App	3102	13.4	0.2	20	1	US-09-021-701-726	Sequence 726, App
c3030	13.4	0.2	20	1	US-08-202-990-3	Sequence 3, Appl1	c3103	13.4	0.2	20	1	US-09-021-701-1069	Sequence 1069, Ap
3031	13.4	0.2	20	1	US-07-976-103A-14	Sequence 14, Appl	c3104	13.4	0.2	20	1	US-09-021-701-1070	Sequence 1070, Ap
c3032	13.4	0.2	20	1	US-08-458-393-9	Sequence 9, Appl1	c3105	13.4	0.2	20	1	US-09-021-701-1071	Sequence 1071, Ap
3033	13.4	0.2	20	1	US-08-487-141B-20	Sequence 20, Appl	c3106	13.4	0.2	20	1	US-09-021-701-1072	Sequence 1072, Ap
3034	13.4	0.2	20	1	US-08-255-892-103	Sequence 103, App	c3107	13.4	0.2	20	1	US-09-021-701-1073	Sequence 1074, Ap
3035	13.4	0.2	20	1	US-08-171-718-13	Sequence 13, Appl	c3108	13.4	0.2	20	1	US-09-021-701-1074	Sequence 1074, Ap
c3036	13.4	0.2	20	1	US-08-605-089-18	Sequence 18, Appl	c3109	13.4	0.2	20	1	US-09-488-857B-46	Sequence 46, Appl
c3037	13.4	0.2	20	1	US-08-665-966-16	Sequence 16, Appl	c3110	13.4	0.2	20	1	US-09-487-368A-81	Sequence 81, Appl
3038	13.4	0.2	20	1	US-08-473-481-14	Sequence 14, Appl	3111	13.4	0.2	20	1	US-09-489-869-61	Sequence 61, Appl
c3039	13.4	0.2	20	1	US-08-621-100-15	Sequence 15, Appl	3112	13.4	0.2	20	1	US-09-489-869-62	Sequence 62, Appl
3040	13.4	0.2	20	1	US-08-117-952-142	Sequence 142, App	3113	13.4	0.2	20	1	US-09-240-473-7	Sequence 7, Appl1
3041	13.4	0.2	20	1	US-08-117-952-148	Sequence 148, App	c3114	13.4	0.2	20	1	US-09-280-590A-5	Sequence 5, Appl1
c3042	13.4	0.2	20	1	US-08-651-692-10	Sequence 10, Appl	c3115	13.4	0.2	20	1	US-08-957-351-17	Sequence 17, Appl
c3043	13.4	0.2	20	1	US-08-927-561-20	Sequence 20, Appl	c3116	13.4	0.2	20	1	US-09-019-160-50	Sequence 50, Appl
c3044	13.4	0.2	20	1	US-08-761-243C-10	Sequence 10, Appl	3117	13.4	0.2	20	1	US-08-984-709A-41	Sequence 41, Appl
c3045	13.4	0.2	20	1	US-08-478-178A-115	Sequence 115, App	3118	13.4	0.2	20	1	US-09-657-042A-73	Sequence 73, Appl
c3046	13.4	0.2	20	1	US-08-488-177-115	Sequence 115, App	c3119	13.4	0.2	20	1	US-08-829-637A-115	Sequence 115, App
c3047	13.4	0.2	20	1	US-08-481-072A-115	Sequence 115, App	c3120	13.4	0.2	20	1	US-09-232-346-56	Sequence 56, Appl
c3048	13.4	0.2	20	1	US-08-664-336-115	Sequence 115, App	3121	13.4	0.2	20	1	US-09-629-645A-24	Sequence 24, Appl
c3049	13.4	0.2	20	1	US-08-866-650-7	Sequence 7, Appl1	3122	13.4	0.2	20	1	US-09-561-497-74	Sequence 74, Appl
c3050	13.4	0.2	20	1	US-08-256-426B-116	Sequence 116, App	c3123	13.4	0.2	20	1	US-09-561-497-75	Sequence 75, Appl
3051	13.4	0.2	20	1	US-08-975-211-27	Sequence 27, App	c3124	13.4	0.2	20	1	US-09-702-251-67	Sequence 67, Appl
3052	13.4	0.2	20	1	US-08-756-806A-15	Sequence 15, Appl	c3125	13.4	0.2	20	1	US-09-175-658B-5	Sequence 5, Appl1
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c3054	13.4	0.2	20	1	US-08-343-443B-119	Sequence 119, App	3127	13.4	0.2	20	1	US-09-689-255C-2	Sequence 2, Appl
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c3056	13.4	0.2	20	1	US-08-507-032-5	Sequence 5, Appl1	3129	13.4	0.2	20	1	US-09-798-096-49	Sequence 49, Appl
3057	13.4	0.2	20	1	US-08-874-186-48	Sequence 48, Appl	c3130	13.4	0.2	20	1	US-09-844-634-45	Sequence 45, Appl
c3058	13.4	0.2	20	1	US-08-940-350-9	Sequence 9, Appl1	c3131	13.4	0.2	20	1	US-09-658-679A-31	Sequence 31, Appl
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; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
; US-08-068-747-6

Query Match 0.3%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 5
; US-08-068-747-11/c
; Sequence 11, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; DESCRIPTION: /desc = "Synthetic"
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Query Match 0.3%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 30 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 2

RESULT 6
; US-08-863-639A-30
; Sequence 30, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-30

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Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 7
US-09-135-994-4
; Sequence 4, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Rannum et al.
; TITLE OF INVENTION: SCAT GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-994-4

Query Match 0.3%; Score 25.8; DB 1; Length 30;
Best Local Similarity 93.1%; Pred. No. 30;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 8
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; Sequence 4, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Rannum et al.
; TITLE OF INVENTION: SCAT GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-684-843A-4

Query Match 0.3%; Score 25.8; DB 1; Length 30;
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Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 9
US-08-570-155-14
; Sequence 14, Application US/08570155
; Patent No. 5962332
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.

;; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
;; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FISH & RICHARDSON P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: U.S.A.
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: #1.30B
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/570,155
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/399,499
;; FILING DATE: 07 March 1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/214,823
;; FILING DATE: 17 March 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 06353/011001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 542-5070
;; TELEFAX: (617) 542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-570-155-14

Query Match 0.3%; Score 25.8; DB 1; Length 31;
Best Local Similarity 93.1%; Pred. No. 32;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7407 CAACATCAGCAGCAGCAGCAGCAGCA 7435
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29

RESULT 10
PCT-US95-02861-14
; Sequence 14, Application PC/TUS9502861
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE
; TITLE OF INVENTION: REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version
SOFTWARE: #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02861
FILING DATE: 08 March 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,823
FILING DATE: 17 March 1994
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 06353/010W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Query Match 0.3%; Score 25.8; DB 1; Length 31;
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Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCA 29
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RESULT 11
US-08-068-747-7
Sequence 7, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Houseman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-7
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RESULT 12
US-08-863-639A-31
Sequence 31, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matsun, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel Wordperfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muech
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-31

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RESULT 13
US-08-113-646A-42/C
Sequence 42, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
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1 APPLICANT: PICKUP, David J.
2 APPLICANT: PATEL, Dhavalumar
3 APPLICANT: ANTCAZAK, James B.
4 TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
5 NUMBER OF SEQUENCES: 44
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: NIXON & VANDERHVE P.C.
8 STREET: 1100 NORTH GLEBE ROAD
9 CITY: ARLINGTON
10 STATE: VIRGINIA
11 COUNTRY: U.S.A.
12 ZIP: 22201-4714
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14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.25
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/113,646A
22 FILING DATE: 31-AUG-1993
23
24 CLASSIFICATION: 435
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26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/084,406
28 FILING DATE: 10-AUG-1987
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: WILSON, MARY J.
32 REGISTRATION NUMBER: 32,955
33 REFERENCE/DOCKET NUMBER: 1579-20
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (703) 816-4000
36 TELEFAX: (703) 816-4100
37
38 TELEX: 200797 NIXN UR
39 INFORMATION FOR SEQ ID NO: 42:
40
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 25 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46
47 MOLECULE TYPE: RNA (genomic)
48
49 US-08-113-646A-42
50
51 Query Match 0.3%; Score 23.4; DB 1; Length 25;
52 Best Local Similarity 96.0%; Pred. No. 58;
53 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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55 Oy 4465 TTTTTTTTTTTTTTTGCTTG 4489
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: APPLICATION NUMBER: US/08/465,384
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Kerner, Ann-Louise
: REGISTRATION NUMBER: 33,523
: REFERENCE/DOCKET NUMBER: HYZ-011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-330-1300
: TELEFAX: 617-330-1311
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 33 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: YES
US-08-465-384-4

Query Match      0.3%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 1,1e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy      4450 TGGGTGCATGCACTTTTTTTTTTTTTTTTTT 4482
          |||||  |||||  |||||  |||||  |||||
Db      1 TGGGTGCAGAGATTTTTTTTTTTTTTTTTTTT 333

RESULT 15
US-08-455-627-12/c
: Sequence 12, Application US/08455627
: Patent No. 5571677
: GENERAL INFORMATION:
: APPLICANT: Sergei M. Gryaznov
: TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
: TITLE OF INVENTION: Connected Macromolecular Structures
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward LLP
: STREET: Five Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94306-2155
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,627
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Nakamura, Jackie N.
: REGISTRATION NUMBER: 35,966
: REFERENCE/DOCKET NUMBER: LYNK-003/01 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-843-5000
: TELEFAX: 415-857-0663
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 30 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
US-08-455-627-12

Query Match      0.3%; Score 23.2; DB 1; Length 30;
Best Local Similarity 89.3%; Pred. No. 95;

```



```

RESULT 19
US-09-466-138-26
; Sequence 26, Application US/09466138
; Patent No. 6153738
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, Richard
; APPLICANT: Oliveira, Baidomero M.
; TITLE OF INVENTION: Contryphan Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rochwell, Figs, Ernst & Kurz, P.C.
; STREET: 755 Thirteenth Street N.W., Suite 701-E
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09466,138
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/061,026
; FILING DATE:
; APPLICATION NUMBER: US 60/068,737
; FILING DATE: 24-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 2314-133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; US-09-466-138-26

Query Match      0.3%; Score 23.2; DB 1; Length 33;
Best Local Similarity 89.3%; Pred. No. 1.2e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      4461 GACCTTTTCTTTTCTTTTCTT 4488
Db      1 GGCCTTTTCTTTTCTTTTCTT 28

RESULT 20
5478746-1/c
; Patent No. 5478746
; APPLICANT: COHEN, JEFFREY I., PURCELL, ROBERT H., FEINSTONE,
; STEPHEN M., ITTEHIRST, JOHN R.
; TITLE OF INVENTION: CDNA ENCODING ATTENUATED CELL CULTURE
; ADAPTED HEPATITIS A VIRUS GENOME
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,646
; FILING DATE: 13-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 789,640
; FILING DATE: 12-NOV-1991
; APPLICATION NUMBER: 462,916
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 88,220

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: FILING DATE: 24-AUG-1987
: APPLICATION NUMBER: 905,146
: FILING DATE: 09-SEP-1986
: APPLICATION NUMBER: 652,067
: FILING DATE: 19-SEP-1984
: APPLICATION NUMBER: 366,165
: FILING DATE: 07-APR-1982
: SEQ ID NO:1
: LENGTH: 33
548746-1
Query Match      0.3%; Score 23.2; DB 1; Length 33;
Best Local Similarity 89.3%; Pred. No.1.2e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY      4463 CTTTTTTTTTTTTTTTTTGTCTGA 4490
DB      29 CTTTTTTTTTTTTTTTTTAAAA 2

RESULT 21
US-08-863-639A-94
: Sequence 94, Application US/08863639A
: Patent No. 5981185
: GENERAL INFORMATION:
: APPLICANT: Matson, Robert S.
: APPLICANT: Coaselin, Peter J.
: APPLICANT: Rampal, Jang B.
: APPLICANT: Caskey, C. T.
: TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
: NUMBER OF SEQUENCES: 95
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sheldon & Mak
: STREET: 225 South Lake Avenue, 9th Floor
: CITY: Pasadena
: STATE: CA
: COUNTRY: USA
: ZIP: 91101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
: COMPUTER: IBM compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: Corel Wordperfect 8 version
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/863,639A
: FILING DATE: May 28, 1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Joseph E. Muech
: REGISTRATION NUMBER: 20,532
: REFERENCE/DOCKET NUMBER: 11859-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (626) 796-4000
: TELEFAX: (626) 795-6321
: INFORMATION FOR SEQ ID NO: 94:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 24 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Other nucleic acid
US-08-863-639A-94

Query Match      0.3%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      7413 CAGCAGCAGCAGCAGCAGCA 7435
DB      2 CAGCAGCAGCAGCAGCAGCA 24

RESULT 22

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US-08-621-914A-3
; Sequence 3, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKUYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE III, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-621-914A-3

Query Match          0.3%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 83;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTTG 4489
DB 1 TTTTGTCTTG 26

RESULT 23
US-10-003-998A-7/c
; Sequence 7, Application US/10003998A
; Patent No. 6664064
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR
; TITLE OF INVENTION: Products
; FILE REFERENCE: 5438/00/EP
; CURRENT APPLICATION NUMBER: US/10/003,998A
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-998A-7

Query Match          0.3%; Score 22.8; DB 1; Length 29;
Best Local Similarity 92.3%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4464 TTTTGTCTTG 4489
DB 26 TTTTGTCTTG 1

RESULT 24
US-08-173-489C-20
; Sequence 20, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C.-G.
; APPLICANT: HEBBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44MB storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from n-myc
; DESCRIPTION: sequence region in Seq ID No. 586124419
; HYPOTHETICAL: yes
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 20 :FROM 1 TO 35
US-08-173-489C-20

Query Match          0.3%; Score 22.8; DB 1; Length 35;
Best Local Similarity 92.3%; Pred. No. 1.6e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTTG 4489
DB 4 TTTTGTCTTG 29

RESULT 25
US-09-244-794A-8/c
; Sequence 8, Application US/09244794A
; Patent No. 6214553
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
```

```

; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/244,794A
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-27
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-794A-8

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GCACCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 29 GGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 26
US-09-007-005-8/c
; Sequence 8, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihne
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-8

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GCACCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 29 GGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 27
US-09-247-190-8/c
; Sequence 8, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
```

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; APPLICANT: Liu, Rihne
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/247,190
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-21
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-8

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GCACCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 29 GGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 28
US-09-244-796-8/c
; Sequence 8, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szoestak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihne
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-796-8

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GCACCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 29 GGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 29
US-09-238-710-8/c
; Sequence 8, Application US/09238710A
; Patent No. 6518018
```

```
; GENERAL INFORMATION:
; APPLICANT: Szoetek, Jack W.
; APPLICANT: Robert, Richard W.
; APPLICANT: Liu, Rihel
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350004
; CURRENT APPLICATION NUMBER: US/09/238,710A
; EARLIER FILING DATE: 1999-01-28
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-238-710-8

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4460 GGACTTTTGTCTTGTCTT 4488
Db      29 GGTTTTGTCTTGTCTTGTCTT 1

RESULT 30
US-09-282-734-3/c
; Sequence 3, Application US/09282734A
; Patent No. 6537749
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002
; CURRENT APPLICATION NUMBER: US/09/282,734A
; CURRENT FILING DATE: 1999-03-03
; EARLIER APPLICATION NUMBER: 60/080,686
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin
US-09-282-734-3

Query Match          0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.1e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4460 GGACTTTTGTCTTGTCTT 4488
Db      29 GGTTTTGTCTTGTCTTGTCTT 1

RESULT 31
US-09-750-401-10
; Sequence 10, Application US/09750401
; Patent No. 6635422
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Carson, Craig C.
; APPLICANT: Tenenbaum, Scott A.

; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; FILE REFERENCE: RBN-001
; CURRENT APPLICATION NUMBER: US/09/750,401
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of GADD45
US-09-750-401-10

Query Match          0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 11.1%; Pred. No. 1.7e+02;
Matches 3; Conservative 21; Mismatches 3; Indels 0; Gaps 0;

QY      4464 TTTTGTCTTGTCTTGTCTTGA 4490
Db      5 UUUUUUUUUUUUUUUUUUUUUUUU 31

RESULT 32
US-10-003-998A-4/c
; Sequence 4, Application US/10003998A
; Patent No. 6664064
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR
; FILE REFERENCE: 5438/00/EP
; CURRENT APPLICATION NUMBER: US/10/003,998A
; CURRENT FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-998A-4

Query Match          0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4464 TTTTGTCTTGTCTTGTCTTGA 4490
Db      32 TTTTGTCTTGTCTTGTCTTGTCTTGA 6

RESULT 33
US-09-527-345-6
; Sequence 6, Application US/09527345
; Patent No. 6334413
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZS163 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/527,345
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-527-345-6

Query Match 0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.2e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCTG 4489
DB 1 TTTTGTCTGCTGCTG 26

RESULT 34
US-09-167-513-10
Sequence 10, Application US/09167513
Patent No. 6388064
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Blumberg, Hal
TITLE OF INVENTION: A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A
FILE REFERENCE: 97-63
CURRENT APPLICATION NUMBER: US/09/167,513
CURRENT FILING DATE: 1998-10-06
EARLIER APPLICATION NUMBER: US 60/061,712
EARLIER FILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-167-513-10

Query Match 0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.2e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCTG 4489
DB 1 TTTTGTCTGCTGCTG 26

RESULT 35
US-09-161-939A-43
Sequence 43, Application US/09161939A
Patent No. 6486299
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Genes and Proteins Predictive and Therapeutic for
FILE REFERENCE: 15966-527
CURRENT APPLICATION NUMBER: US/09/161,939A
CURRENT FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: oligo(dT)<25>V
US-09-161-939A-43

Query Match 0.3%; Score 22; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.2e+02;
Matches 23; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCTG 4489
DB 1 TTTTGTCTGCTGCTG 26

RESULT 36
US-09-325-554-18
Sequence 18, Application US/09325554
Patent No. 6410235
GENERAL INFORMATION:
APPLICANT: Weindel, Kurt
APPLICANT: Brand, Joachim
TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX
FILE REFERENCE: 024420-00008
CURRENT APPLICATION NUMBER: US/09/325,554
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 198-24-900.4
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent-In version 3.1
SEQ ID NO 18
LENGTH: 27
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
NAME/KEY: misc signal
LOCATION: (27)-(27)
OTHER INFORMATION: Y means incorporation of Amino linker-phosphoramidite subsequent
US-09-325-554-18

Query Match 0.3%; Score 22; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTCTGCT 4487
DB 4 TTTTGTCTGCTGCT 27

RESULT 37
US-08-068-747-2/c
Sequence 2, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
FILE REFERENCE: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

```

: LENGTH: 30 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: DESCRIPTION: /desc = "synthetic"
:
US-08-068-747-2

```

Query Match	0.3%	Score 22;	DB 1;	Length 30
Best Local Similarity	83.3%	Pred. No. 1.6e+02;		
Matches 25; Conservative	0;	Mismatches 5;	Indels	

Qy 51 CGGCGGCGAAGGAGCTCGGGGGCGGCGG 8
Db 30 CGGCGGCGGCGGCGGCGGCGGCGGCGG 1

RESULT 38
US-09-268-505B-13
; Sequence 13, Application US/09268505B
Date: 09/10/2010

```

?
? TITLE OF INVENTION: Method for Enrichment of Unique DNA Fragments
? TITLE OF INVENTION: through Cyclical Removal of PCR Adaptor Attached to DNA
? TITLE OF INVENTION: Fragments whose Sequences Are Shared Between Two DNA Pools
?
? FILE REFERENCE: 3-11-99
?
? CURRENT APPLICATION NUMBER: US/09/268,505B
?
? CURRENT FILING DATE: 1999-03-11
?
? PRIOR APPLICATION NUMBER: none
?
? PRIOR FILING DATE: N/A
?
? NUMBER OF SEQ ID NOS: 15
?
? SOFTWARE: Microsoft word
?

```

```

; ORGANISM: synthetic
; FEATURE:
; NAME/KEY: oligo d(T)
; LOCATION:
US-09-268-505B-13

```

Query Match	0.3%	Score 22	DB 1	Length 31
Best Local Similarity	88.5%	Pred. No. 1.7e+02		
Matches 23; Conservative	1	Mismatches 2	Indels 0	Gaps 0

QY 4464 TTTTITTTTTTTTTTTTTTGTCCTG 4489
 |||||
Db 6 TTTTITTTTTTTTTTTTTTTTTTV 31
 |||||

```

RESULT 39
US-08-341-148-2
: Sequence 2, Application US/08341148
: Patent No. 5610287
:
: GENERAL INFORMATION:
: APPLICANT: NIKIFOROV, THEO
: APPLICANT: KNAPP, MICHAEL
: TITLE OF INVENTION: METHOD FOR THE IMMOBILIZATION OF NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HOWREY & SIMON
: STREET: 1299 PENNSYLVANIA AVENUE, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,148
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AUBRACH, JEFFREY I
REGISTRATION NUMBER: 32,690
REFERENCE/DOCKET NUMBER: 699-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Equus caballus
IMMEDIATE SOURCE:
CLONE: Biotin-T25
US-08-341-148-2

Query Match          0.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred.No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Ox      4464 TTTTTTTTTTTTTTTTGTCTT 4488
db      1 TTTTTTTTTTTTTTTTTTTT 25

```

RESULT 40-130-2
 Sequence 2, Application US/08460130
 Patent No. 5734020
 GENERAL INFORMATION:
 APPLICANT: yuán N. wóng
 TITLE OF INVENTION: Production and Use
 TITLE OF INVENTION: of Magnetic Porous Inorganic Materials
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CPG, Inc.
 STREET: 3 Borinski Road
 CITY: Lincoln Park
 STATE: New Jersey
 COUNTRY: United States of America
 ZIP: 07035
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3M Double Density
 MEDIUM TYPE: 5 1/4" diskette
 COMPUTER: Wang PC
 OPERATING SYSTEM: MS DOS Version
 OPERATING SYSTEM: 3.20
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,130
 FILING DATE: 2 June 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/307,307
 FILING DATE: 16 September 1994
 APPLICATION NUMBER: 07/794,910
 FILING DATE: 20 No. 5734020ember 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Irons, Edward S.
 REGISTRATION NUMBER: 16,541
 REFERENCE/DOCKET NUMBER: Wóng
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 626-3564

REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: Wong
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 626-3564


```

; TITLE OF INVENTION: METHOD FOR THE IMMOBILIZATION OF NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14096
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 639-105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Equus caballus
; IMMEDIATE SOURCE:
; CLONE: Biotin-T25
; PCT-US94-14096-2

Query Match          0.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTGTGCTT 4488
Db      1 TTTTGTGCTT 25

RESULT 45
US-08-621-914A-1
; Sequence 1, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKIYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
```

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; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE IIT, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; US-08-621-914A-1

Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTGTGCTT 4488
Db      1 TTTTGTGCTT 25

RESULT 46
US-08-621-914A-2
; Sequence 2, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKIYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; TITLE OF INVENTION: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE IIT, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; US-08-621-914A-2

Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 4464 TTTTGTCTT 4488
DB 1 TTTTGTCTT 25

RESULT 47

US-08-873-437-2
Sequence 2, Application US/08873437
Patent No. 6124092
GENERAL INFORMATION:
APPLICANT: O'Neill, Roger A.
APPLICANT: Chen, Jer-Kang
APPLICANT: Chiesa, Claudia
APPLICANT: Fry, George
TITLE OF INVENTION: Multiplex Polynucleotide Capture
TITLE OF INVENTION: Methods and Compositions
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: PE Applied Biosystems
STREET: 850 Lincoln Centre Drive
CITY: Foster City
STATE: CA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,437
FILING DATE: 12-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,832
FILING DATE: 04-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: 4294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-638-6245
TELEFAX: 415-638-6071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-873-437-2

Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTT 4488
DB 1 TTTTGTCTT 25

RESULT 48
US-09-197-951-5
Sequence 5, Application US/09197951
Patent No. 6197554
GENERAL INFORMATION:
APPLICANT: LIN, SHI-LUNG
APPLICANT: CHENG-WING
YING, SHAO-YAO
TITLE OF INVENTION: Method for Generating Full-Length cDNA
Library from Single Cells
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: David & Raymond Patent Firm

STREET: 108 N. Ynez Ave., Suite 128
CITY: Monterey Park
STATE: CA
COUNTRY: USA
ZIP: 91754
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,951
FILING DATE: 20-NO. 6197554-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chan, Raymond Y.C.
REGISTRATION NUMBER: 37,484
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 571-9812
TELEFAX: (626) 571-9813
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
HYPOETHERICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-197-951-5

Query Match 0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTT 4488
DB 1 TTTTGTCTT 25

RESULT 49
US-09-522-217-38
Sequence 38, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 26
TYPE: DNA


```

; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-295-723-38

Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTTGTGCTT 4488
Db      1 TTTTGTGCTT 25

RESULT 57
US-10-295-723-39
; Sequence 39, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764b
US-10-295-723-39

Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTTGTGCTT 4488
Db      1 TTTTGTGCTT 25

RESULT 58
US-08-208-486-79/c
; Sequence 79, Application US/08208486
; Patent No. 5389531
; GENERAL INFORMATION:
; APPLICANT: Ito, Junetsu
; APPLICANT: Yoo, Seung-Ku
; TITLE OF INVENTION: METHODS TO REPLICATE DNA IN VITRO USING
; TITLE OF INVENTION: PRD1-CATALYZED DNA REPLICATION SYSTEMS
; NUMBER OF SEQUENCES: 89
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cabill, Sutton & Thomas
; STREET: 155 Park One, 2141 E. Highland Ave.
; CITY: Phoenix
; STATE: Arizona
; COUNTRY: U.S.A.
; ZIP: 85016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
; COMPUTER: Packard Bell (IBM PC/AT compatible)
; OPERATING SYSTEM: MS-Dos, Version 5.0
; SOFTWARE: WordPerfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,486
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,916
; FILING DATE: April 14, 1992
; APPLICATION NUMBER: Japan 240525/91
; FILING DATE: August 26, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janelle Faunce Raupp
; REGISTRATION NUMBER: 30,485
; REFERENCE/DOCKET NUMBER: #3954-A-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602) 956-7000
; TELEFAX: (602) 495-9475
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-208-486-79

Query Match          0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTTGTGCTT 4488
Db      27 TTTTGTGCTT 3

RESULT 59
US-09-475-947A-153
; Sequence 153, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 27
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-153

Query Match          0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTTGTGCTT 4488
Db      2 TTTTGTGCTT 26
```

RESULT 60
US-08-433-505-9/C
Sequence 9, Application US/08433505
Patent No. 5695936
GENERAL INFORMATION:
APPLICANT: MANDRAND, Bernard
APPLICANT: CROS, Philippe
APPLICANT: DELAIR, Thierry
APPLICANT: CHARLES, Marie-Helene
APPLICANT: BROU, Marie-No. 569593611e
APPLICANT: PICHOT, Christian
APPLICANT: TONNELIER, Jean-Claude
TITLE OF INVENTION: REAGENT AND METHOD FOR THE DETECTION OF
A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,505
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36349
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-433-505-9

Query Match 0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTT 4488
|||||
30 TTTTGTCTT 6

Db 30 TTTTGTCTT 6

RESULT 61
US-08-870-730-9/C
Sequence 9, Application US/08870730
Patent No. 6017707
GENERAL INFORMATION:
APPLICANT: MANDRAND, Bernard
APPLICANT: CROS, Philippe
APPLICANT: DELAIR, Thierry
APPLICANT: CHARLES, Marie-Helene
APPLICANT: BROU, Marie-No. 601770711e
APPLICANT: PICHOT, Christian
TITLE OF INVENTION: REAGENT AND METHOD FOR THE DETECTION OF
A NUCLEOTIDE SEQUENCE WITH SIGNAL AMPLIFICATION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:

ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,730
FILING DATE: 06-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36349A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-870-730-9

Query Match 0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTT 4488
|||||
30 TTTTGTCTT 6

Db 30 TTTTGTCTT 6

RESULT 62
US-09-083-123-3
Sequence 3, Application US/09083123
Patent No. 6326143
GENERAL INFORMATION:
APPLICANT: Orum, Hendrik
APPLICANT: Seeger, Corina
TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
Acids
FILE REFERENCE: sequence listing
CURRENT APPLICATION NUMBER: US/09/083,123
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: EP 95118600.6
EARLIER FILING DATE: 1995-11-25
EARLIER APPLICATION NUMBER: PCT/EP96/05149
EARLIER FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-3

Query Match 0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTT 4488
|||||
1 TTTTGTCTT 25

Db 1 TTTTGTCTT 25

```

RESULT 63
US-09-083-123-7/c
; Sequence 7, Application US/09083123
; Patent No. 6326143
; GENERAL INFORMATION:
; APPLICANT: Orum, Hendrik
; APPLICANT: Seeger, Corina
; TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
; TITLE OF INVENTION: Acids
; FILE REFERENCE: sequence listing
; CURRENT APPLICATION NUMBER: US/09/083,123
; CURRENT FILING DATE: 1998-05-22
; EARLIER APPLICATION NUMBER: EP 95118600.6
; EARLIER FILING DATE: 1995-11-25
; EARLIER APPLICATION NUMBER: PCT/EP96/05149
; EARLIER FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-7
Query Match          0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred.No.1.8e+02;
Matches      23; Conservative    0; Mismatches     2; Indels       0; Gaps        0,

Cy      4464 TTTTYYYYTTTTTTTTTGTCCT 4488
           |||||
Db      30   TTTTYYYYTTTTTTTTTTTTTTT 6

RESULT 64
US-08-882-649A-10/c
; Sequence 10, Application US/08882649A
; Patent No. 6344316
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; Chee, Mark
; Gunderson, Kevin
; Chaogiang, Lai
; Wodicka, Lisa
; Cronin, Maureen T.
; Lee, Danny
; Tran, Huu M.
; Matsuzaki, Hajime
; Mcgall, Glenn H.
TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joe Liebeschuetz
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,649A
FILING DATE: 25-Jun-1997
CLASSIFICATION: 435-006.000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,471
FILING DATE: 23-JAN-1996

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; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US77/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
;
US-08-882-649A-10
;
Query Match          0.3% Score 21.6; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      4464 TTTTGTGTTTTTTTGTCCTT 4488
       |||||
Db       30 TTTTGTGTTTTTTTGTCCTT    6

RESULT 65
US-09-648-040-4/C
; Sequence 4, Application US/09648040
; Patent No. 643665
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; FILE REFERENCE: 50036/032002
; CURRENT APPLICATION NUMBER: US/09/648,040
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,261
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Encoding molecule
; NAME/KEY: misc_feature
; LOCATION: 10
; ;
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-09-648-040-4
Query Match          0.3% Score 21.6; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      4460 GGACTTTTGTGTCCTT 4488
       |||||
Db       30 GGTTTGTGTTTTTTTNTTTT    2

RESULT 66
US-09-475-947A-134
; Sequence 134, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.

```



```

; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 134
; LENGTH: 24
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-134

Query Match      0.3%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4464 TTTTGTCTGTC 4486
Db 2 TTTTGTCTGTC 24

RESULT 67
US-09-721-154-4
; Sequence 4, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Valberg, Eugeni
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; FILE REFERENCE: CYCOP007C2
; CURRENT APPLICATION NUMBER: US/09/721,154
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Paused-sequence
US-09-721-154-4

Query Match      0.3%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4463 CTTTGTCTGTC 4485
Db 1 CTTTGTCTGTC 23

RESULT 68
US-08-910-632-5/c
; Sequence 5, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
; APPLICANT: KOOL, ERIC T.
; TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
; FILE REFERENCE: 220.00010130
; CURRENT APPLICATION NUMBER: US/08/910,632B
; CURRENT FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 08/805,631
; EARLIER FILING DATE: 1997-02-26
; EARLIER APPLICATION NUMBER: 08/393,439
; EARLIER FILING DATE: 1995-02-23
; EARLIER APPLICATION NUMBER: 08/047,860
```

```

; EARLIER FILING DATE: 1993-04-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic AS83 DNA nanocircle
US-08-910-632-5

Query Match      0.3%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.7e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4464 TTTTGTCTGCTG 4489
Db 26 TTTTGTCTGCTG 1

RESULT 69
US-08-805-631A-5/c
; Sequence 5, Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; FILE REFERENCE: DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RASCH & GEBHARDT, P.A.
; STREET: 119 No. 6096880th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,631A
; FILING DATE: 26-FEB-97
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-805-631A-5

Query Match      0.3%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.7e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4464 TTTTGTCTGCTG 4489
Db 1 TTTTGTCTGCTG 1
```

Db 26 TTTT TTTT TTTT G TTTT TTTT TTTT G 1

RESULT 70
US-09-569-344-5/c
; Sequence 5, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
; DNA
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 No. 6368802th Fourth Street, Suite 201
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,344
; FILING DATE: 11-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/805,631
; FILING DATE: 26-FEB-97
; APPLICATION NUMBER: US 08/393,439
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: US 08/047,860
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDBERG, VICTORIA A.
; REGISTRATION NUMBER: 41,287
; REFERENCE/DOCKET NUMBER: 220.00010140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1226
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-569-344-5

Query Match 0.3%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1.7e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT G C T G 4469
Db 26 TTTT TTTT TTTT G TTTT TTTT TTTT G 1

RESULT 71
US-09-304-232-152
; Sequence 152, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypermethylation

; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APOA4 3058
US-09-304-232-152

Query Match 0.3%; Score 21.2; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 2.1e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7405 AGCAACATCAGCAGCAGCAGCAGCA 7432
Db 2 AGCAGAGACGACGACGAGCAGCAGCA 29

RESULT 72
PCT-US92-10792-1
; Sequence 1, Application PC/TUS9210792
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha D.
; APPLICANT: Johnston, Brian H.
; TITLE OF INVENTION: Triplet Helix Formation at
; TITLE OF INVENTION: (PunPyn)-(PunPyn) Tracts
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI International
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10792
; FILING DATE: 19921211
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,934
; FILING DATE: 21-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-3141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: OLIGONUCLEOTIDE I, FIGURE 8
PCT-US92-10792-1

REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-40

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7414 AGCAGCAGCAGCAGCAGCAGC 7434
DB 1 AGCAGCAGCAGCAGCAGCAGC 21

RESULT 76
US-08-863-639A-60/c
Sequence 60, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-60

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7433
DB 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 77
US-08-863-639A-66
Sequence 66, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

Query Match 0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCAGCA 7435
DB 1 GCAGCAGCAGCAGCAGCAGCA 21

RESULT 78
US-08-863-639A-69/c
Sequence 69, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

```

;
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
;
US-08-863-639A-69

Query Match          0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7414 AGCAGCAGCAGCAGCAGCAGC 7434
Db      21 AGCAGCAGCAGCAGCAGCAGC 1

RESULT 79
US-08-863-639A-87/c
; Sequence 87, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Watson, Robert S.
; APPLICANT: Coasain, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
;
US-08-863-639A-87
```

```

US-08-863-639A-87

Query Match          0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7415 GCAGCAGCAGCAGCAGCAGCA 7435
Db      21 GCAGCAGCAGCAGCAGCAGCA 1

RESULT 80
US-08-400-275-13
; Sequence 13, Application US/08400275
; Patent No. 5668295
; GENERAL INFORMATION:
; APPLICANT: Wahab, Samir Z.
; APPLICANT: Malik, Vedpal S.
; TITLE OF INVENTION: PUTRESCINE N-METHYLTRANSFERASE.
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING PUTRESCINE
; TITLE OF INVENTION: N-METHYLTRANSFERASE, AND TRANSGENIC TOBACCO PLANTS WITH
; TITLE OF INVENTION: ALTERED NICOTINE CONTENT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Ave. of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,275
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,681
; FILING DATE:
; APPLICATION NUMBER: US 07/613,160
; FILING DATE: 14-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: PM-1696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
;
US-08-400-275-13

Query Match          0.3%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4463 CTTTCTTTCTTTCTTTCTTTCTTTT 4483
Db      9 CTTTCTTTCTTTCTTTCTTTT 29

RESULT 81
US-08-227-476-5/c
```

```
; Sequence 5, Application US/08227476
; Patent No. 6498025
; GENERAL INFORMATION:
; APPLICANT: Miller, Jeffrey E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CDNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray, Cary, Ames & Frye
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/989,851
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weseman, James C.
; REGISTRATION NUMBER: 39,507
; REFERENCE/DOCKET NUMBER: P0023US0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-3604
; TELEFAX: (619) 236-1048
; TELEX: 910-335-1273
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-227-476-5

Query Match          0.3%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4463 CTTTTTTTTTTTTTTTTTTT 4483
Db      21 CTTTTTTTTTTTTTTTTTTT 1

RESULT 82
US-09-475-947A-332
; Sequence 332, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 332
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-332

Query Match          0.3%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.5e+02;
```

```
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      52 GCGCGAAGCAGCTGCGGGCGCGG 80
Db      1 GCGCGCGCGCGCGCGCGCGCGG 29

RESULT 83
US-08-522-623-14
; Sequence 14, Application US/08522623
; Patent No. 5585242
; GENERAL INFORMATION:
; APPLICANT: Khalil, Omar S.
; APPLICANT: Bouma, Stanley R.
; APPLICANT: Pabich, Edward K.
; TITLE OF INVENTION: METHOD AND DEVICE FOR DETECTION OF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,623
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,839
; FILING DATE:
; APPLICATION NUMBER: US/07/863,553
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brainard, Thomas D.
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5158.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-4864
; TELEFAX: (708) 937-9556
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 32
US-08-522-623-14

Query Match          0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4463 CTTTTTTTTTTTTTTTTTTT 4483
Db      12 CTTTTTTTTTTTTTTTTTTT 32

RESULT 84
US-09-619-103-14/C
; Sequence 14, Application US/09619103
; Patent No. 6429300
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
```

```

1  APPLICANT:  lohse, peter
2  APPLICANT:  Wagner, Richard
3  TITLE OR INVENTION:  Peptide Acceptor Ligation Methods
4  FILE REFERENCE:  50036/031002
5  CURRENT APPLICATION NUMBER:  US/09/619,103
6  CURRENT FILING DATE:  2000-07-19
7  PRIOR APPLICATION NUMBER:  60/145,834
8  PRIOR FILING DATE:  1999-07-27
9  NUMBER OF SEQ ID NOS:  26
10 SOFTWARE:  PaatSeq for Windows Version 4.0
11 SEQ ID NO 14
12     LENGTH:  32
13     TYPE:  RNA
14     ORGANISM:  Artificial Sequence
15     FEATURES:
16     OTHER INFORMATION:  designed sequence to act as a linker
17     US-09-619-103-14

```

Query March	0.3%	Score 21;	DB 1;	Length 32;
Best Local Similarity	100.0%	Pred. No. 2.9e+02;		
Matches 21;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	4464	TTTTTTTTTTTTTTTTTTTTTTTG	4484
Db	30	TTTTTTTTTTTTTTTTTTTTTTTG	10

```

PCT-US93-03256-14
RESULT 85
Sequence 14, Application PC/TUS9303256
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: METHOD AND DEVICE FOR DETECTION OF
TITLE OF INVENTION: NUCLEIC ACID OR ANALYTE USING TOTAL INTERNAL REFLECTION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: United States of America
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin and Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03256
FILING DATE: 19930506
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/863,553
FILING DATE: 06 APRIL 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brainard, Thomas D.
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5158, .US 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
TELEFAX: (708) 937-2623
INFORMATION FOR SEQ ID NO.: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 32
PCT-US93-03256-14

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Query Match	0.3%	Score 21;	DB 1;	Length 32;
Best Local Similarity	100.0%	Pred. No. 2.9e+02;		
Matches 21; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

```

RESULT 86
US-08-014-943A-25/c
; Sequence 25, Application US/08014943A
; Patent No. 5545551
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPICANT: Bergemann, Andrew D.
TITLE OF INVENTION: Cloning And Expression Of PUR Protein
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
City: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,943A
FILING DATE: 02/FEB/1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-014-943A-25

Query Match          0.3%; Score 20.8; DB 1; Length 24
Best Local Similarity 91.7%; Pred.No.1.7e+02;
Matches    22; Conservative   0; Mismatches    2; Indels

QY      4464 TTTTGTGCTTGGTCT 4487
Db       24 TTTTTTTTTTTTTTTTTTTT 1

```

[illegible]

RESULT 87
US-08-486-421-50/c
Sequence 50, Application US/08486421
Patent No. 5672479
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSES: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-486-421-50

Query Match	0.3%	Score 20.8;	DB 1;	Length 24;
Best Local Similarity	91.7%;	Pred. No. 1.7e+02;		
Matches 22; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

OY	4464	TTTTTTTTTTTTTTTTTGGCT	4487
Db	24	TTTTTTTTTTTTTTTTTTTTTTT	1

RESULT 88
US-08-470-911-50/C
Sequence 50, Application US/08470911
Patent No. 5756684
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470, 911
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30, 742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

```

; TELIX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 50::
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-470-911-50

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Query Match	0.3%	Score 20.8;	DB 1;	Length 24;
Best Local Similarity	91.7%;	Pred. No. 1.7e+02;		
Matches 22;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy	4464	TTTTTTTTTTTTTTTTTTGTC	4487
Db	24	TTTTTTTTTTTTTTTTTTTTT	1

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Query Match	0.3%;	Score 20.8;	DB 1;	Length 24;
Best Local Similarity	91.7%;	Pred. No. 1.7e+02;		
Matches 22;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY	4464	TTTTTTTTTTTTTTTTTTGCT	4487
D6	24	TTTTTTTTTTTTTTTTTTTTT	1

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US-08-486-809-50/c
US-08-486-809-50/c
: Sequence 50, Application US/08486809
: Patent No. 5869622
: GENERAL INFORMATION:
: APPLICANT: Johnson, Edward M.
: APPLICANT: Bergemann, Andrew D.
: TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
: NUMBER OF SEQUENCES: 51
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/486, 809
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/470,911
: FILING DATE: 06-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 6923-053
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9030
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 24 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-486-809-50

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4464 TTTTTTTTTTTTTTTTGTCT 4487
Db 24 TTTTTTTTTTTTTTTTTTTT 1

RESULT 91
US-09-183-619-7/c
: Sequence 7, Application US/09183619
: Patent No. 6103474
: GENERAL INFORMATION:
: APPLICANT: DELINGER, DOUGLAS J.
: APPLICANT: DAHM, SUEANN C.
: APPLICANT: ILSLEY, DIANE D.
: APPLICANT: ACH, ROBERT A.
: APPLICANT: TROLL, MARK A.
: TITLE OF INVENTION: HYBRIDIZATION ASSAY SIGNAL ENHANCEMENT
: FILE REFERENCE: 10981619-1
: CURRENT APPLICATION NUMBER: US/09/183,619
: CURRENT FILING DATE: 1998-10-30
: EARLIER APPLICATION NUMBER: 08/735,381
: EARLIER FILING DATE: 1996-10-21
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.0

```

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; SEQ ID NO 7
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: poly A-RNA target
US-09-183-619-7

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTNTTTTTTTTTTTGCTC 4487
          |||||
          24 TTTTNTTTTTTTTTTTTTTTT 1

RESULT 92
US-09-201-674-1/C
; Sequence 1, Application US/09201674
; Patent No. 6110682
; GENERAL INFORMATION:
APPLICANT: Dellinger, Douglas J.
           Dahm, SueAnn
           Troll, Mark
TITLE OF INVENTION: SIGNAL ENHANCEMENT METHOD AND KIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hewlett-Packard Company, Legal Dept.,
           Palo Alto
STREET: 1501 Page Mill Road, MS 4U-10
STATE: California
CITY: Palo Alto
COUNTRY: USA
ZIP: 94304-1126
COMPUTER READABLE FORM.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,674
FILING DATE: 30-No. 6110682-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,381
FILING DATE: 21-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10950427-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-857-4125
TELEFAX: 650-852-8063
TELEX: 348-461
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: mRNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-201-674-1

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTNTTTTTTTTTTTGCTC 4487

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Db      24 TTTTTTTTTTTTTTTTTTTT 1

RESULT 93
US-09-536-936-11/c
; Sequence 11, Application US/09536936
; Patent No. 6346384
; GENERAL INFORMATION:
; APPLICANT: Pollner, Reinhold
; TITLE OF INVENTION: Real Time Monitoring of PCR Using LOCI
; FILE REFERENCE: BEH-7438
; CURRENT APPLICATION NUMBER: US/09/536,936
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide attached to beads
US-09-536-936-11

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTGTCT 4487
Db      24 TTTTTTTTTTTTTTTTTTTT 1

RESULT 94
US-09-025-639-4/c
; Sequence 4, Application US/09025639
; Patent No. 6365346
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurich
; APPLICANT: Patel, Rajesh D.
; TITLE OF INVENTION: Quantitative Determination of Nucleic
; FILE REFERENCE: BEH-7408
; CURRENT APPLICATION NUMBER: US/09/025,639
; CURRENT FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(24)
; OTHER INFORMATION: Synthetic DNA Probe
US-09-025-639-4

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTGTCT 4487
Db      24 TTTTTTTTTTTTTTTTTTTT 1

RESULT 95
US-09-333-237-4/c
; Sequence 4, Application US/09333237
; Patent No. 6406667
; GENERAL INFORMATION:
; APPLICANT: Singh, Sharat
; APPLICANT: Ullman, Edwin F.
```

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; TITLE OF INVENTION: Chemiluminescent Compositions For Use In
; TITLE OF INVENTION: Detection Of Multiple Analyses
; FILE REFERENCE: BEH-7383A
; CURRENT APPLICATION NUMBER: US/09/333,237
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 09/025,624
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: detection probe bound to sensitizer particle
US-09-333-237-4

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTGTCT 4487
Db      24 TTTTTTTTTTTTTTTTTTTT 1

RESULT 96
US-09-732-067-1/c
; Sequence 1, Application US/09732067
; Patent No. 6457426
; GENERAL INFORMATION:
; APPLICANT: Ullman, Edwin
; APPLICANT: Singh, Rajendra
; APPLICANT: Deketzer, Steve
; APPLICANT: Davalian, Darloush
; TITLE OF INVENTION: Amplified Luminescent Homogeneous
; FILE REFERENCE: BEH-7385
; CURRENT APPLICATION NUMBER: US/09/732,067
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hybridization oligo
US-09-732-067-1

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTGTCT 4487
Db      24 TTTTTTTTTTTTTTTTTTTT 1

RESULT 97
US-10-043-415-4/c
; Sequence 4, Application US/10043415
; Patent No. 6573054
; GENERAL INFORMATION:
; APPLICANT: Kurn, Nurich
; APPLICANT: Patel, Rajesh D.
; TITLE OF INVENTION: Quantitative Determination of Nucleic
; FILE REFERENCE: BEH-7408
; CURRENT APPLICATION NUMBER: US/10/043,415
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/09/025,639
; PRIOR FILING DATE: 1998-02-18
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; Sequence 19, Application US/08123449A
; Patent No. 5583032
; GENERAL INFORMATION:
; APPLICANT: TORENC, PAUL
; APPLICANT: ROBERT, SILVERMAN
; APPLICANT: RATAN, MAITRA
; APPLICANT: KRSTYNA, LESTAK
; TITLE OF INVENTION: METHOD OF CLEANING SPECIFIC SEQUENCES
; TITLE OF INVENTION: OF RNA
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS version
; SOFTWARE: FastSeq Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,449A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10103
; FILING DATE: 10-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pedrick, Michael F.
; REGISTRATION NUMBER: 36,799
; REFERENCE/DOCKET NUMBER: NIH034.0010PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 1-4
; OTHER INFORMATION: A is linked by 2',5'-linkage
; FEATURE:
; NAME/KEY: miscellaneous feature
; LOCATION: 4
; OTHER INFORMATION: A is linked at 2' end to following
; OTHER INFORMATION: base through a linker moiety
; US-08-133-449A-19
;
; Query Match 0.3%; Score 20.4; DB 1; Length 22;
; Best Local Similarity 95.5%; Pred. No.1.7e+02;
; Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 4464 TTTTTTTTTTTTTTTTTTTT 4485
; DB 22 TTTTTTTTTTTTTTTTTTTT 1
;
; RESULT 102
; US-08-458-050-19/c
; Sequence 19, Application US/08458050
; Patent No. 5677289
; GENERAL INFORMATION:
; APPLICANT: TORENC, PAUL
; APPLICANT: ROBERT, SILVERMAN
;

```

```

APPLICANT: RATAN, MAITRA
TITLE OF INVENTION: METHOD OF CLEANING SPECIFIC SEQUENCES
TITLE OF INVENTION: METHOD OF RNA
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS version
SOFTWARE: FastSeq Version 1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,050
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,449
FILING DATE: 17-SEP-1993
APPLICATION NUMBER: PCT/US93/10103
FILING DATE: 10-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH034,001QPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: miscellaneous feature
LOCATION: 1-4
OTHER INFORMATION: A is linked by 2',5'-linkage
US-08-458-050-19
Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred.No.1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY      4464 TTTT TTTTTTTTTTTTTTTGT 4485
Db      22 TTTT TTTTTTTTTTTTTTTTTT 1

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1  TITLE OF INVENTION:  COMPOSITIONS AND METHODS OF USE OF
2  TITLE OF INVENTION:  MAMMALIAN RETROTRANSPOSONS
3  NUMBER OF SEQUENCES:  137
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
6  STREET:  ONE CONGRESS SQUARE, 2005 MARKET STREET, 2ND FL.
7  CITY:  PHILADELPHIA
8  STATE:  PA
9  COUNTRY:  U.S.A.
10 ZIP:  19103-7086
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE:  Floppy disk
13 COMPUTER:  IBM PC compatible
14 OPERATING SYSTEM:  PC-DOS/MS-DOS
15 SOFTWARE:  Patent In Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  US/08/847,844A
18 FILING DATE:  28-APR-1997
19 CLASSIFICATION:  800
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER:  US 08/749,805
22 FILING DATE:  16-NOV-1996
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:  US 60/006,831
25 FILING DATE:  16-NOV-1995
26 ATTORNEY/AGENT INFORMATION:
27 NAME:  DOYLE LEARY Ph.D., KATHRYN
28 REGISTRATION NUMBER:  36,317
29 REFERENCE/DOCKET NUMBER:  9596-2302
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE:  215-567-2020
32 TELEFAX:  215-567-2991
33 INFORMATION FOR SEQ ID NO:  94:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH:  22 base pairs
36 TYPE:  nucleic acid
37 STRANDEDNESS:  single
38 TOPOLOGY:  linear
39 MOLECULE TYPE:  RNA (genomic)
40 US-08-847-844A-94
41
42 Query Match      0.3%; Score 20.4; DB 1; Length 22;
43 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
44 Matches 21, Conservative 0, Mismatches 1, Indels 0, Gaps 0;
45
46 Oy      4464 TTTTTTTTTTTTTTTTTTCT 4485
47 Db      22 TTTTTTTTTTTTTTTTTT 1
48
49 RESULT 104
50 US-08-950-196-19/c
51 Sequence 19, Application US/08950196
52 Patent No. 6271369
53 GENERAL INFORMATION:
54 APPLICANT:  TORRENCE, PAUL
55 APPLICANT:  ROBERT, SILVERMAN
56 APPLICANT:  RATAN, MAITRA
57 APPLICANT:  KRISTYNA, LESIAK
58 TITLE OF INVENTION:  METHOD OF CLEAVING SPECIFIC SEQUENCES
59 TITLE OF INVENTION:  OF RNA
60 NUMBER OF SEQUENCES:  22
61 CORRESPONDENCE ADDRESS:
62 ADDRESSEE:  Knobbe, Martens, Olson and Bear
63 STREET:  620 Newport Center Drive
64 CITY:  Newport Beach
65 STATE:  CA
66 COUNTRY:  USA
67 ZIP:  92660
68 COMPUTER READABLE FORM:
69 MEDIUM TYPE:  Diskette
70 COMPUTER:  IBM Compatible
71 OPERATING SYSTEM:  DOS version

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1 SOFTWARE: FastSeq Version 1.0
2
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/950.196
5 FILING DATE:
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US/08/123.449
8 FILING DATE:
9 APPLICATION NUMBER: PCT/US93/10103
10 FILING DATE: 10-OCT-1993
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Fredrick, Michael P.
13 REGISTRATION NUMBER: 36,799
14 REFERENCE/DOCKET NUMBER: NIH034.0010PC
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 714-760-0404
17 TELEFAX: 714-760-9502
18 INFORMATION FOR SEQ ID NO: 19:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 22 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: CDNA
25 HYPOTHETICAL: NO
26 ANTI-SENSE: NO
27 FRAGMENT TYPE:
28 ORIGINAL SOURCE:
29 FEATURE:
30 NAME/KEY: miscellaneous feature
31 LOCATION: 1-4
32 OTHER INFORMATION: A is linked by 2', 5'-linkage
33 FEATURE:
34 NAME/KEY: miscellaneous feature
35 LOCATION: 4
36 OTHER INFORMATION: A is linked at 2' end to following
37 OTHER INFORMATION: base through a linker moiety
38 US-08-950-196-19
39
40 Query Match 0.3%; Score 20.4; DB 1; Length 22;
41 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
42 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
43
44 QY 4464 TTTTTTTTTTTTTTTTTTGT 4485
45 |||||||||||||||
46 Db 22 TTTTTTTTTTTTTTTTTT 1
47
48 RESULT 105
49 US-09-720-201A-25/c
50 ; Sequence 25, Application US/09720201A
51 ; Patent No. 6524853
52 GENERAL INFORMATION:
53 APPLICANT: KOHARA, MICHINORI
54 APPLICANT: KOHARA, KYOKO
55 APPLICANT: TAIRA, KAZUNARI
56 APPLICANT: MATSUZAKI, JUNICHI
57 APPLICANT: OHNORI, HIROSHI
58 TITLE OR INVENTION: A VECTOR EXPRESSING AN RNA VIRAL FULL-LENGTH GENE AND
59 TITLE OF INVENTION: ITS USE
60 FILE REFERENCE: 04853.0051-00000
61 CURRENT APPLICATION NUMBER: US/09/720.201A
62 CURRENT FILING DATE: 2000-12-22
63 PRIOR APPLICATION NUMBER: JP 96/177,820
64 PRIOR FILING DATE: 1998-06-24
65 PRIOR APPLICATION NUMBER: PCT/JP99/03381
66 PRIOR FILING DATE: 1999-06-24
67 NUMBER OF SEQ ID NOS: 25
68 SOFTWARE: PatentIn Ver. 2.1
69 SEQ ID NO 25
70 LENGTH: 22
71 TYPE: DNA
72 ORGANISM: Artificial Sequence
73 FEATURE:

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; OTHER INFORMATION: Description of Artificial Sequence: Poly A
; OTHER INFORMATION: nucleotide sequence
US-09-720-201A-25

Query Match          0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTGTGTGTGTGTGTGTGTGT 4485
DB 22 TTTTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 106
US-09-721-154-6
; Sequence 6, Application US/09721154
; Patent No. 6651008
; GENERAL INFORMATION:
; APPLICANT: Vaisberg, Eugene
; APPLICANT: Adams, Cynthia
; APPLICANT: Sabry, James
; APPLICANT: Crompton, Anne
; TITLE OF INVENTION: Database system including computer code
; TITLE OF INVENTION: for predictive cellular bioinformatics
; FILE REFERENCE: CytoP007C2
; CURRENT APPLICATION NUMBER: US/09/721,154
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/311,996
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pseudo-sequence
US-09-721-154-6

Query Match          0.3%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4467 TTTTGTGTGTGTGTGTGTGTGTGTGT 4488
DB 2 TTTTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 107
US-08-117-361C-3
; Sequence 3, Application US/08117361C
; Patent No. 573223
; GENERAL INFORMATION:
; APPLICANT: Venkatakrishna, Shyamala
; APPLICANT: Tekamp-Olson, Patricia
; TITLE OF INVENTION: Endocheilin B1 (ETB1) Receptor Polypeptide
; TITLE OF INVENTION: Compositions, Methods, and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 946087
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 &
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,361C
```

```
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Ling-Fong
; REGISTRATION NUMBER: 36,482
; REFERENCE/DOCKET NUMBER: 0945.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2704
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-117-361C-3

Query Match          0.3%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4460 GACCTTTTGTGTGTGTGTGTGTGTGT 4481
DB 5 GACCTTTTGTGTGTGTGTGTGTGTGT 26

RESULT 108
US-08-666-405-15
; Sequence 15, Application US/0866405
; Patent No. 5874220
; GENERAL INFORMATION:
; APPLICANT: FACH, Patrick; GUILLOU,
; APPLICANT: Jean-Pierre; POPOFF, Michel
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: AMPLIFICATION OF GENES CODING FOR THE
; TITLE OF INVENTION: ENTEROTOXIN AND THE LECTININASE OF CLOSTRIDIUM
; TITLE OF INVENTION: PERFRINGENS AND THEIR APPLICATION TO THE
; TITLE OF INVENTION: DETECTION AND NUMERATION OF THESE BACTERIAE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,405
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/04292
; FILING DATE: 22-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/172,026
; FILING DATE: 22-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 102.164
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
```


INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-569-344-6

Query Match 0.3%; Score 20.2; DB 1; Length 29;
Best Local Similarity 88.0%; Pred. No. 3.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTGTGTTTGTGTTT 4488
DB 5 TTTTGTGTTTGTGTTTGTGTTT 29

RESULT 112
US-08-146-504-16
Sequence 16, Application US/08146504
Patent No. 5605662
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; and Tu, Eugene
TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
TITLE OF INVENTION: DIAGNOSTICS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,504
FILING DATE: No. 5605662ember 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: none
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waibury, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-146-504-16

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTGTGTTTGTGTTT 4483
DB 5 TTTTGTGTTTGTGTTTGTGTTT 29

DB 1 TTTTGTGTTTGTGTTTGTGTTT 20

RESULT 113
US-08-379-593-5
Sequence 5, Application US/08379593
Patent No. 5849480
GENERAL INFORMATION:
APPLICANT: Cros, Philippe
APPLICANT: Kurfurst, Robin
APPLICANT: Batelli, Nicole
APPLICANT: Piga, Nadia
TITLE OF INVENTION: HAPTEN ASSAY DEVICE AND USE THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLTF & BERRIDGE
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk, 1.44M storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,593
FILING DATE: 02-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPA 36056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "SYNTHETIC DNA"
FEATURE:
OTHER INFORMATION: consists of nucleosides with an alpha anomer and carries
US-08-379-593-5

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTGTGTTTGTGTTT 4483
DB 1 TTTTGTGTTTGTGTTTGTGTTT 20

RESULT 114
US-08-725-976-16
Sequence 16, Application US/08725976
Patent No. 5929208
GENERAL INFORMATION:
APPLICANT: Heller, Michael J.; and Tu, Eugene
TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: WINDOWS (VERSION 3.0)
SOFTWARE: WordPerfect (Version 6.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,976
FILING DATE: October 4, 1996
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 5929208ember 1, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 222/211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-725-976-16

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 115
US-08-997-080-83/c
Sequence 83, Application US/0897080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-08-997-080-83

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 116
US-08-997-362-83/c
Sequence 83, Application US/0897362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Miyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
US-08-997-362-83

Query Match 0.3%; Score 20; DB 1; Length 20;


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# CURRENT FILING DATE: 1999-02-12
# NUMBER OF SEQ ID NOS: 12
# SOFTWARE: PatentIn Ver. 2.1
# SEQ ID NO 1
# LENGTH: 20
# TYPE: DNA
# ORGANISM: Artificial Sequence
# FEATURE:
# NAME/KEY: misc feature
# LOCATION: (1) - (19)
# OTHER INFORMATION: 2'-methoxyethoxy (MOE)
# OTHER INFORMATION: Description of Artificial Sequence: No. 6207819e1
# OTHER INFORMATION: Sequence
# US-09-250-075-1

```

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches	20;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 4464 4483
1 20
Db

RESULT 123
US-09-173-936B-14
; Sequence 14, Application US/09173936B
; Patent No. 6238865
; GENERAL INFORMATION:
; APPLICANT: Zhen, Huang, Szostak, Jack W.
; TITLE OF INVENTION: A Simple and Efficient Method to Label and Modify 3'-
; Terminal
; of RNA Using DNA Polymerase and a Synthetic Template with D
; Nucleotides

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cohen, Pontani, Lieberman
STREET: 551 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10176

COMPUTER READABLE FORM:
MEDIA TYPE: 3.50 inch Diskette
COMPUTER: IBM-MS
OPERATING SYSTEM: Window 95
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173, 936B
FILING DATE: 16-Oct-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/063,757
FILING DATE: 17-OCT-1997

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
    LENGTH: 20 bases
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-173-936B-14

```

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.6e+02;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy	4464	4483
Db	1	20

```

RESULT 124
US-09-454-704A-13/c
: Sequence 13. Application US/09454704A
: Patent No. 6274321
:
: GENERAL INFORMATION:
: APPLICANT: Blumberg, Bruce
: TITLE OF INVENTION: High Throughput Functional Screening of
: TITLE OF INVENTION: CDNAs
: FILE REFERENCE: P-DC 3662
: CURRENT APPLICATION NUMBER: US/09/454,704A
: CURRENT FILING DATE: 1999-12-03
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 20
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: cDNA
US-09-454-704A-13

```

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.6e+02;		
Matches	20;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY	4464		4483
Db	20		1

```

RESULT 125
US-09-324-542-83/C
/ Sequence 83, Application US/09324542
/ Patent No. 6328978
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Tan, Paul L.J.
/ APPLICANT: Prestidge, Ross
/ TITLE OF INVENTION: Methods and Compounds for the Treatment
/ TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
/ FILE REFERENCE: 11000.1007C1
/ CURRENT APPLICATION NUMBER: US/09/324,542
/ CURRENT FILING DATE: 1999-06-02
/ EARLIER APPLICATION NUMBER: US 08/997,080
/ EARLIER FILING DATE: 1997-12-23
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 83
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Made in a lab
US-09-324-542-83

```

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.6e+02;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

[illegible]

RESULT 126
 US-09-205-426-83/c
 ; Sequence 83, Application US/09205426
 ; Patent No. 6406704
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L. J.
 ; TITLE OF INVENTION: Compounds and Methods for Treatment and
 ; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

```

1 FILE REFERENCE: 11000.1002c34
2 CURRENT APPLICATION NUMBER: 09/09/205, 426
3 CURRENT FILING DATE: 1998-12-04
4 EARLIER APPLICATION NUMBER: 09/095, 855
5 EARLIER FILING DATE: 1998-06-11
6 EARLIER APPLICATION NUMBER: 06/997, 362
7 EARLIER FILING DATE: 1997-12-23
8 EARLIER APPLICATION NUMBER: 08/873, 970
9 EARLIER FILING DATE: 1997-06-12
10 EARLIER APPLICATION NUMBER: 08/705, 347
11 EARLIER FILING DATE: 1996-08-29
12 NUMBER OF SEQ ID NOS: 208
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ ID NO 83
15 LENGTH: 20
16 TYPE: DNA
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Made in a lab
20 US-09-205-426-83

```

Query Match	0.3%	Score 20	DB 1	Length 20
Best Local Similarity	100.0%	Pred. No.	1.6e+02	
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	4464	4483
20		
Db		

RESULT 127
 US-09-619-103-26/C
 Sequence 26. Application US/09619103
 Patent No. 6423300
 GENERAL INFORMATION:
 APPLICANT: Kurtz, Markus
 APPLICANT: Lohse, Peter
 APPLICANT: Wagner, Richard
 TITLE OF INVENTION: Peptide Acceptor Ligation Methods
 FILE REFERENCE: 50036/031002
 CURRENT APPLICATION NUMBER: US/09/619,103
 CURRENT FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 60/145,834
 PRIOR FILING DATE: 1999-07-27
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 26
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURES:
 OTHER INFORMATION: designed sequence for nucleic acid purification
 US-09-619-103-26

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.Ce+02;		
Matches 20; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy		4464	T T T T T T T T T T T T T T T T T	4483
Dz	20	T T T T T T T T T T T T T T T T T		1

```

RESULT 128
US-09-726-096A-1
: Sequence 1, Application US/09726096A
: Patent No. 6462184
: GENERAL INFORMATION:
: APPLICANT: Manoharan, Muthiah
: APPLICANT: Maier, Martin A.
: TITLE OF INVENTION: Compounds And Intermediates For Synthesis Of Mixed Back
: TITLE OF INVENTION: Oligomeric Compounds
: FILE REFERENCE: 1S1S4528

```

```

? CURRENT APPLICATION NUMBER: US/09/726,096A
?
? CURRENT PILING DATE: 2000-11-29
?
? NUMBER OF SEQ ID NOS: 12
?
? SOFTWARE: PatentIn version 3.0
?
? SEQ ID NO 1
?
? LENGTH: 20
?
? TYPE: DNA
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? NAME/KEY: misc feature
?
? OTHER INFORMATION: Oligonucleotide
?
? NAME/KEY: misc feature
?
? LOCATION: (1)..(20)
?
? OTHER INFORMATION: 2'-methoxyethoxy (MOE)
?
US-09-726-096A-1

```

Query Match 0.3%; Score No. DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4464	4483
Db	1	20

```

RESULT 129
US-09-603-830-55/C
; Sequence 55, Application US/09603830
; Patent No. 6506564
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 4149-1-1-1-1
; CURRENT APPLICATION NUMBER: US/09/603,830
; CURRENT FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; TYPE: DNA
; LENGTH: 20
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
; US-09-603-830-55

```

Query Match	0.3%	Score 20	DB 1	Length 20
Best Local Similarity	100.0%	Pred. No.	1.6e+02	
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	4464	4483
20		
Db		

RESULT 130
US-09-976-978A-55/c


```

; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-491A-55
```

```
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db      20 TTTT TTTT TTTT TTTT TTTT TTTT 1
```

```

RESULT 134
US-09-957-313A-55/c
; Sequence 55, Application US/09957313A
; Patent No. 6645721
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghamian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-13
; CURRENT APPLICATION NUMBER: US/09/957,313A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-957-313A-55
```

```
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db      20 TTTT TTTT TTTT TTTT TTTT TTTT 1
```

```

RESULT 135
US-09-966-312-55/c
; Sequence 55, Application US/09966312
; Patent No. 6673548
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghamian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-15
; CURRENT APPLICATION NUMBER: US/09/966,312
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-966-312-55
```

```
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db      20 TTTT TTTT TTTT TTTT TTTT TTTT 1
```

```

RESULT 136
US-09-975-062A-55/c
; Sequence 55, Application US/0975062A
; Patent No. 6677122
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghamian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-111
; CURRENT APPLICATION NUMBER: US/09/975,062A
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
```

```
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-975-062A-55
```

```
Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4464 TTTT TTTT TTTT TTTT TTTT 4483
Db      20  TTTT TTTT TTTT TTTT TTTT 1
```

```
RESULT 137
US-09-976-971A-55/c
; Sequence 55, Application US/09976971A
; Patent No. 6682895
; GENERAL INFORMATION:
; APPLICANT: Mitkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storchoff, James J.
; APPLICANT: Elghamian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; FILE REFERENCE: 00-713-118
; CURRENT APPLICATION NUMBER: US/09/976,971A
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/603,830
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Microsoft Word 2000
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-976-971A-55
```

```
Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4464 TTTT TTTT TTTT TTTT TTTT 4483
```

```
Db      20  TTTT TTTT TTTT TTTT TTTT 1
```

```
RESULT 138
PCT-US93-07603-6/c
; Sequence 6, Application PC/TUS9307603
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: NUCLEIC ACID RECOGNITION AND TRANSPORT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07603
; FILING DATE: 19930813
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,087
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0636/7007W0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Synthetic RNA oligonucleotide.
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US93-07603-6
```

```
Query Match          0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4464 TTTT TTTT TTTT TTTT TTTT 4483
Db      20  TTTT TTTT TTTT TTTT TTTT 1
```

```
RESULT 139
US-08-146-504-2/c
; Sequence 2, Application US/08146504
; Patent No. 5605662
; GENERAL INFORMATION:
; APPLICANT: Heller, Michael J.; and Tu, Eugene
; TITLE OF INVENTION: SELF-ADDRESSABLE SELF-ASSEMBLING
; TITLE OF INVENTION: MICROELECTRONIC SYSTEMS AND DEVICES FOR
; TITLE OF INVENTION: MOLECULAR BIOLOGICAL ANALYSIS AND
; TITLE OF INVENTION: DIAGNOSTICS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
```

STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,504
FILING DATE: No. 5605662ember 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
APPLICATION NUMBER: described below:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 203/218
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-146-504-2

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 140
US-08-455-896-13
Sequence 13, Application US/08455896
Patent No. 5668267
GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL, & HAFERRAMP
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
ZIP: 63105-1817
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,896
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 952726
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-455-896-13

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 141
US-08-933-149-13
Sequence 13, Application US/08933149
Patent No. 5922836
GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
TITLE OF INVENTION: MAMMARY-SPECIFIC BREAST CANCER PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL, & HAFERRAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
ZIP: 63105-1817
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,149
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: HENDERSON, MELDIE W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-933-149-13

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 142
US-08-725-976-2/c
Sequence 2, Application US/08725976
Patent No. 5929208
GENERAL INFORMATION:
APPLICANT: Heller, Michael J. and Tu, Eugene
TITLE OF INVENTION: METHODS FOR ELECTRONIC SYNTHESIS OF POLYMERS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: WINDOWS (VERSION 3.0)
SOFTWARE: WordPerfect (Version 6.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,976
FILING DATE: October 4, 1996
CLASSIFICATION: 422
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/146,504
FILING DATE: No. 5929208ember 1, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, David B.
REGISTRATION NUMBER: 31,125
REFERENCE/DOCKET NUMBER: 222/211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-725-976-2

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 143
US-09-082-343-13
Sequence 13, Application US/09082343
Patent No. 5968754
GENERAL INFORMATION:
APPLICANT: WATSON, MARK A.
APPLICANT: FLEMING, TIMOTHY P.
TITLE OF INVENTION: DNA SEQUENCE AND ENCODED
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROGERS, HOWELL & HAFERKAMP
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105-1817

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,343
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,896
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 952726
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-082-343-13

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 144
US-08-863-639A-10/c
Sequence 10, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muehl
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
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TELEFAX: (626) 795-6321